



From: Sent:

Mertz, Prema

Tuesday, July 05, 2005 2:37 PM STIC-Biotech/ChemLib

To: Subject:

10/751,242

Please search SEQ ID NO:1-2 with protein databases.

Thanks.

Prema Mertz, Ph.D. Prema Mertz, Pri.D.
Primary Examiner
Art Unit 1646
4D81 Remsen Bldg Mailbox 4C70
US Patent & Trademark Office
Tel # (571) 272-0876
FAX # (571) 273-0876

**********
STAFF USE ONLY
Searcher:
Searcher Phone: 2-
Date Searcher Picked up:
Date Completed:
Searcher Prep/Rev. Time:
Online Time:

\_\_\_\_AA#:\_\_\_\_ :\_\_\_\_ SPDI:\_ NA#:\_ Interference: SPD S/L: Oligomer: S/L:\_\_ Encode/Transl: Structure#:\_\_\_ \_ Text: Inventor:\_\_\_\_ Litigation:\_\_\_\_

\*\*\*\*\*\*\*\* Type of Search

******
endors and cost where applicable
STN:
DIALOG:
QUESTEL/ORBIT:
LEXIS/NEXIS:
SEQUENCE SYSTEM:
WWW/Internet:
Other(Specify):

š

```
Minimum
Maximum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Result
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 s
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Database
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                               ĕ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB DB
                                                                                                                                           110.5
108.5
106.5
101
96
96
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score
    94.5
94.5
99.55
88.55
88.55
88.55
                                                                                                                                                                                                                                                         738
734
727
702
641
634
511
304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      seq length:
seq length:
  Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1612378 seqs, 512079187 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gapop 10.0 ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BLOSUM62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-10-751-242-1
896
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        July
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    UniProt_03:*
1: uniprot_sprot:*
2: uniprot_trembl:;*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TPLGPASSLPQSFLLKCLEQ.....SHLQSFLEVSYRVLRHLAQP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Copyright
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9, 2005, 12:25:44; Search time 110.682 Seconds
(without alignments)
805.025 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2000000000
 174
175
195
195
208
211
211
211
208
189
189
189
189
2175
2175
2175
2175
2175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GenCore version (c) 1993 - 2005
                                                                                                                                                                                                                                                                                                                                                                                                                                                               멂
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gapext 0.5
              Q8MKE5
HMCU_DROME
Q9A523
Q9I019
Q8RJY3
                                                                                                                            Q9H2A5
IL6_FELCA
Q8D706
                                                                                                                                                                      IL6_PIG
IL6_ORCOR
IL6_HORSE
Q6NZ82
                                                                                                                                                                                                                                                                                                                Q9GJU0
CSF3_SHEEP
CSF3_CANFA
CSF3_BOVIN
CSF3_PIG
CSF3_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                   Q8N4W3
CSF3_HUMAN
CSF3_FELCA
                                                                                    Q9NPF7
Q6NZ80
                                                                                                                                                                                                                           Q90VI0
Q8MJ75
Q9XT80
                                                                                                                                                                                                                                                                        Q8MKE0
MGF_CHICK
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ħ
                                                                                                                29KTL6
LL6_BOVIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Compugen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ltd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1612378
                                                        Q8mke5
P10180
                                                                                                                            P41683
Q8d706
                                                                                                                                                                                                                                             Q8mj
                                                                                                                                                                                                                                                           Z90Y
                                           Q9a523
                                                                                                                Q9kt
                                                                                                                                                          Q9h2a5
                                                                                                                                                                                     Q95181
                                                                                                                                                                         Q6nz82
                                                                                                                                                                                                                                                                           P13854
                                                                                                                                                                                                                                                                                                                                                                                                                    P09919
                                                                                                                                                                                                                                                                                                                                                                                                                                 Q8n4w3 homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Description
                                                                                                               felis silve
vibrio vuln
vibrio chol
                                                                                                                                                      sus scrofa
delphinapte
sus scrofa
crimus orc
equus cabal
homo sapien
homo sapien
                                                                                                                                                                                                                                                        rattus norv
equus cabal
egallus gall
gallus gall
                                                                    homo sapien
homo sapien
sus scrofa
              pseudomonas
stigmatella
                                           caulobacter
                                                        drosophila
                                                                                                                                                                                                                                                                                                                   Bull
                                                                                                                                                                                                                                                                                                                                           bos taurus
                                                                                                                                                                                                                                                                                                                                                           canis famil
                                                                                                                                                                                                                                                                                                                                                                          ovis aries
                                                                                                                                                                                                                                                                                                                                                                                      felis silve
                                                                                                                                                                                                                                                                                                                                                                                                   homo sapien
felis silve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       174
                                                                                                                                                                                                                                                                                                                   musculu
                                                                                                                                                                                                                                                                                                                               scrofa
    ALU DRR RELEGIORE RELEGIO DE RESERVA DE RESE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q8N4W3
Q8N4W3;
01-OCT-2002
01-OCT-2002
01-MAR-2004
                                                                                                                                                                                                  rissuB=Skin;
                PF00489;
 PR00433;
```

45	44	43	42	41	40	39	38	37	36	35	34	y S	32
84	84	84.5	84.5	84.5	85	85	85.5	85.5	86	86	96	86	86
9.4	9.4	9.4	9.4	9.4	9.5	9.5	9.5	9.5	9.6	9.6	9.6	9.6	9.6
208	175	455	211	209	208	193	1288	211	852	851	850	788	502
٦	N	N	1	r	N	N	N	N	N	N	N	N	N
IL6_CAPHI	Q9TTH4	Q7MDW7	IL6_LAMGL	IL6_PHOVI	Q6V919	Q9N2H9	Q8LQR8	Q865W7	Q811T9	Q8CF88	Q7TQ21	Q8CF87	Q34008
Q28319 capra hircu	aotus	Q7mdw7 vibrio vuln	Q865x6 lama glama			Q9n2h9 sus scrofa	Q8lqr8 oryza sativ		Q811t9 mus musculu	Bru	Q7tq21 mus musculu	Q8cf87 mus musculu	Q34008 beta vulgar

ALIGNMENTS

## WKEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899; WKEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899; WK Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., WK Lausmer R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., WK Lausmer R.D., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., WA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., WA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., WA Lausmer A.A., Rubin G.M., Hong L., WA Lausmer A.A., Rubin G.M., Hong L., WA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., WA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., WA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., WA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., WA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., WA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., WA Willalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., WA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., WA Villalon D.K., Morriey K.C., Hale S., Garcia A.M., Rodrigues S., Sanchez A., Whitling M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Whitling M., Walshan J.W., Green E.D., Dickson M.C., WA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S., WA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., WA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Strausberg R.; Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases. Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases. EMBL; BE033245; AAH33245.1; RMBL; BE033245; AAH33245.1; RMBC; GO:0005136; C:extracellular; IEA. RGO; GO:0005125; F:cytokine activity; IEA. RGO; GO:0005125; F:interleukin-6 receptor binding; IEA. RGO; GO:0005138; F:interleukin-6 response; IEA. RGO; GO:0005138; F:immune response; IEA. RGO; GO:000515; P:immune response; IEA. RGO; GO:000515; GGEF MGF. R InterPro; IPR003573; II6\_MGF\_GCSF. R InterPro; IPR003573; II6\_MGF\_GCSF. R InterPro; IPR003574; Interleukin\_6. Krzywinski M.A.; Jones S.J., Marra M.A.; Jones S.J., Marra M.A.; "Generation and initial analysis of more than 15, un and mouse CDNA sequences."; and mouse CDNA sequences." Eukaryota; Metazoa; Mammalia; Eutheria; 01-OCT-2002 (TrEMBLrel. 22, 01-OCT-2002 (TrEMBLrel. 22, 01-MAR-2004 (TrEMBLrel. 26, 01-MAR) stimulating factor 3, NCBI\_TaxID=9606; SEQUENCE FROM N.A. SEQUENCE FROM N.A. Homo sapiens (Human) PRELIMINARY; Chordata; Primates; w • Last sequence update) Last annotation updat Created) isoform Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo. PRT; more than 15,000 0 200 A update) databases. full-length humar

IL6GCSFMGF

```
밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ś
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local S
Matches 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3_HUMAN
CSF3_HI
P09919,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRINTS; PR00434; INTERLEUKIN6.
ProDom; PD004388; GCSF MGF; 1.
ProDom; PD004356; Interleukin_6;
SMART; SM00126; IL6; 1.
PROSITE; PS00254; INTERLEUKIN_6;
SEQUENCE 200 AA; 21543 MW; 8
                                                                                                                                                                                                                                            Nagata S., Tsuchiya M., Asano S.,
Oheda M., Nomura H., Yamazaki T.;
                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                 SEQUENCE OF 19-207
MEDLINE=86151684; 1
                                                                                                       SEQUENCE
                                                                                                                                                                     MEDLINE=87196936; Po
Devlin J.J., Devlin
                                                                                                                                                                                                              "The chromosomal gene structure and colony-stimulating factor."; EMBO J. 5:575-581(1986)
                                                                                                                                                                                                                                                                  MEDLINE=86220137; PubMed=2423327;
                                                                                                                                                                                                                                                                                                   "Molecular cloning and expression colony-stimulating factor."; Nature 319:415-418(1986).
                                                                                                                                                                                                                                                                                                                                                          MEDLINE=86118679;
                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Granulocyte
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-MAR-1989
25-OCT-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-MAR-1989
                                                           "SeattleSNPs. N
FHCRC, Seattle,
                                                                                 Nickerson
                                                                                                                                                                                                                                                                                                                                                                                                                                              (Filgrastim)
                                                                                                                                                Expression of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   174;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             μ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEELGMAPALQPTQGAMPAFASAFQRRAGGVLVASHLQSFLEVSYRVLRHLAQP 1.74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LSSCPSQALQLAGCLSQLHSGLFLYQGLLQALEGISPELGPTLDTLQLDVADFATTIWQQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TPLGPASSLPQSFLLKCLEQVRKIQGDGAALQEKLCATYKLCHPEELVLLGHSLGIPWAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TPLGPASSLPQSFLLKCLEQVRKIQGDGAALQEKLCATYKLCHPEELVLLGHSLGIPWAP
                                                                                        FROM N.A., AND VARIANTS MET-157 AND J., Carrington D.P., Chung M.-W., Le
                                                                               D.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEELGMAPALQPTQGAMPAFASAFQRRAGGVLVASHLQSFLEVSYRVLRHLAQP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LSSCPSQALQLAGCLSQLHSGLFLYQGLLQALEGISPELGPTLDTI
                                                (JUN-2001)
                                                                                                                                                                                                                                                                                                                                    Tsuchiya M., Asano S
Kubota N., Oheda M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                       (Rel. 10, Last sequence up (Rel. 45, Last annotation colony-stimulating factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (Rel.
(Rel.
(Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%;
ilarity 100.0%;
Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                       (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                              (Lenograstim)
                                                                                                                                                granulocyte colony-stimulating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
rROM N.A.
1; PubMed=2420009;
e T.C., Gabril
                                                                                                                          41:302-306(1987).
                                                                                                                                                                   PubMed=3494801;
in P.E., Myambo
                                                                                                                                                                                                                                                                                                                                                         PubMed=3484805;
                                                L) (URL:
                                                                                                                                                                                                                                                                                                                                                                                                   Chordata;
Primates;
                                                                     HL66682
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Created)
                                                the
                                              582 program for genomic applications, http://pga.gs.washington.edu)."; http://pga.gs.washington.edu).";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
                                                                                                                                                                                                                                                                                                                        S., Kaziro Y., Yamaz
L., Nomura H., Ono M.;
sion of cDNA for huma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 896; DB 2;
Pred. No. 5.2e-74;
; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                    Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       factor precursor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8648AA55B329A96C
                                                                                                                                                                     <u>.</u>
      J.,
                                                                                                                                                                                                                                                         Yamamoto O.,
                                                                                                                                                                                                                                      two
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               update)
                                                                                                                                                                                                                                                                                                                          cDNA for human
                                                                                                                                                                   Lilly M.B., Rado
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               207
       Lai
                                                                                                                                                                                                                                      mRNAs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A
      P.H.,
                                                                                            Lee
                                                                                           ee K.L.,
                                                                                                                                                                                                                                                                                                                                              Yamazaki T.,
                                                                                                                                                                                                                                      for
                                                                                                                                                factor
                                                                                                                                                                                                                                                         Hirata Y., Kubota
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CRC64;
       Zsebo K.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                          (G-CSF)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length
                                                                                                                                                                                                                                    human granulocyte
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                          granulocyte
                                                                                            Poe1
                                                                                                                                                γď
                                                                                                                                                                      Н
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LQLDVADFATTIWQQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                          (Pluripoietin)
                                                                                                                                                human
                                                                                            C.L.,
                                                                                                                                                                                                                                                                                                                                                 Yamamoto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
                                                                                                                                                cell
                                                                       ă
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                            ĭ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     200
                                                                                                                                                                                                                                                                                                                                               0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               60
```

EMBL;

X03438; M13008; X03656; X03655;

; CAA27168.1; ; AAA03056.1; ; CAA27291.1; ; CAA27290.1;

or send entities

an

non-profit institutions as long and this statement is not removed. requires a license agreement ( an email to license@isb-sib.ch)

(See

http://www.isb-sib.ch/announce/

and

for

commercial

8

as its content

Usage

```
MEDLINE=93106200; PubMed=1281794; DOI=10.1016/0014-5793(92)81521-M; Zink T., Ross A., Ambrosius D., Rudolph R., Holak T.A.; "Secondary structure of human granulocyte colony-stimulating factor derived from NNR spectroscopy."; FEBS Lett. 314:435-439(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Murdock D.C., Chazin V.R., Bruszewski J., Lu H., (Barendt J., Platzer E., Moore M.A.S., Mertelsmann "Recombinant human granulocyte colony-stimulating normal and leukemic myeloid cells.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIINE-93281718; PubMed=7685117;
Hill C.P., Osslund T.D., Elsenberg D.;
"The structure of granulocyte-colony-stimulating relationship to other growth factors.";
Proc. Natl. Acad. Sci. U.S.A. 90:5167-5171(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=94304859; PubMed=7518249;
Zink T., Ross A., Luers K., Cieslar C.,
"Structure and dynamics of the human gra
factor determined by NMR spectroscopy. I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Clogston C.L., Hu S., Boone T.C., Lu H.S.; "Glycosidase digestion, electrophoresis and chromatographic of recombinant human granulocyte colony-stimulating factor groduced in Chinese hamster ovary cells."; J. Chromatogr. A 637:55-62(1993).
                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  factor determined by bundle protein.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRUCTURE BY NMR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CARBOHYDRATE-LINKAGE SITE.
MEDLINE=93293942; PubMed=7685769;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Science
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Biochemistry 33:8453-8463(1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRUCTURE BY NMR.
                                                                                                                                                                                                                                                                             HARMACEUILCHE: AVAILABLE (Ringen/Roche) and Granocyte (Rhone-Poulenc). Used to the (Amgen/Roche) and Granocyte (Rhone-Poulenc). In entropenia (a disorder characterized by an extremely of neutrophils in blood).

SIMILARITY: Belongs to the IL-6 superfamily.

CAUTION: Ref. 4 misquotes the gene name as "CSF1".
                                                                                                                                                                                                                         CAUTION: Ref. 4 misquotes the gene name as "CSFI". DATABASE: NAME=Neupogen/Granulokine; NOTE=Clinical information on Neupogen/Granulokine; WWW="http://www.neupogen.com/".
                                                                                                                                                                                                                                                                                                                                                                    PTM: O-glycan consists of Gal-GalNAc disaccharide which can be modified with up to two sialic acid residues (done in recombinantly expressed G-CSF from CHO cells).

PHARMACEUTICAL: Available under the names Neupogen or Granulokine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUBUNIT: Monomer.
SUBCELLULAR LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 differentiation, and function of 2 of the blood, the granulocytes and
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Name=Short
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FUNCTION: Granulocyte/macrophage colony-stimulating cytokines that act in hematopolesis by controlling
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Event=Alternative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ALTERNATIVE PRODUCTS
                                                                                                                                                                                                                                                                                                                                                                                                                                            IsoId=P09919-2; Sequence=VSP_002673;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IsoId=P09919-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 232:61-66(1986)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    induces granulocytes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                splicing; Named
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Secreted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C., Rudolph R., Holak T.A.;
granulocyte colony-stimulating
y. Loop mobility in a four-heli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  isoforms=2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       related white cell populat
the monocytes-macrophages.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Chen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    n R., Welt
g factor:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Welte
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      effects
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         populations
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           four-helix-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           production,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            glycoforms
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              analysis
                                                                                                                                                                                                                                                                                                                                      number
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8
```

```
RESULT 3
CSF3_FELC
ID CSF3
AC 0027
DT 30-N
DT 30-N
DT 05-U
DE Gran
                                                                                                                                                                                                                                               밁
                                                                                                             Ś
                                                                                                                                문
                                                                                                                                                 Ś
                                                                                                                                                                      밁
                                                                                                                                                                                      δ
                                                                                                                                                                                                          Query Match
Best Local S
Matches 174
                                      CSF3_FE
002708;
                                                                                                                                                                                                                                                                                                                                                                                                                 DISULFID
DISULFID
CARBOHYD
                                                          FELCA
                                                                                                                                                                                                                                                                HELIX
TURN
TURN
HELIX
TURN
TURN
HELIX
TURN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MIM; 138970;
GO; GO:000561
GO; GO:000513
           30-MAY-2000
05-JUL-2004
                              30-MAY-2000
                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                   HELIX
                                                                                                                                                                                                                                                                                                                                                                     VARIANT
                                                                                                                                                                                                                                                                                                                                                                                        VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                        VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                            CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF00489; IL6; 1
PRINTS; PR00433; IL6GCSFMGF.
ProDom; PD008388; GCSF MGF; 1.
SMART; SM00126; IL6; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Growth factor;
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE; PS00254; INTERLEUKIN 6; 1.
3D-structure; Alternative splicing; Cytokine; Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PDB; 1PGR; X-ray; A/C/E/G=30-207.
PDB; 1RHG; X-ray; A/B/C=31-207.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR003573;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Genew;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PIR; A24573; A24573.
PIR; A25093; FQHUGL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GO:0005615;
GO:0005130;
GO:0007275;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GO:0008284;
                                                FELCA
                                                                                                              118
                                                                                              151
                                                                                                                                 91
                                                                                                                                                   58
                                                                                                                                                                     31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AF388025; AAK62469.1;
M17706; AAA35882.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HGNC:2438; CSF3.
                                                                                                                                                                                                                   Similarity
                                                                                                         WQQMBELGMAPALQPTQGAMPAFASAFQRRAGGVLVASHLQSFLEVSYRVLRHLAQP 174
                                                                                                                                            WAPLSSCPSQALQLAGCLSQLHSGLFLYQGLLQALEGISPELGPTLDTLQLDVADFATTI
                                                                                            WQQMEELGMAPALQPTQGAMPAFASAFQRRAGGVLVASHLQSFLEVSYRVLRHLAQP
                                                                                                                                WAPLSSCPSQALQLAGCLSQLHSGLFLYQGLLQALEGISPELGPTLDTLQLDVADFATTI
                                                                                                                                                                    TPLGPASSLPQSFLLKCLEQVRKIQGDGAALQEKLVSECATYKLCHPEELVLLGHSLGIP
                                                                                                                                                                                     TPLGPASSLPQSFLLKCLEQVRKIQGDGAALQEKL---CATYKLCHPEELVLLGHSLGIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IPR003629;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                D8284; P:positive regulation of cell proliferation; TAS
IPR009079; 4_helix_cytokine.
          (Rel. 39,
(Rel. 39,
(Rel. 44,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NMR; @=30-207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             X-ray; A/C=30-207
(Rel. 39, Last sequence update) (Rel. 44, Last annotation updat colony-stimulating factor precu
                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                 41
69
77
105
125
125
130
133
157
                                                                                                                                                                                                                                                                                                                                                                     174
                                                                                                                                                                                                                                                                                                                                                                                      157
                                                                                                                                                                                                                                                                                                                                                                                                        31
69
97
166
                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pharmaceutical;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C:extracellular space; TAS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   F:granulocyte colony-stimulating factor recep. . .; P:development; TAS.
                                                                                                                                                                                                                                                                65
71
86
88
124
127
132
156
158
                                                                                                                                                                                                                                                                                                                                                                                                       207
75
107
166
68
                                                                                                                                                                                                                                                                                                                                                                     174
                                                                                                                                                                                                                                                                                                                                                                                       157
                                                                                                                                                                                                                                               22293
                                                                                                                                                                                                                  98.7%;
98.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           _IL6_MGF_GCSF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4_helix_cytokine.
GCSF_MGF.
                              Created)
                                                                                                                                                                                                                                               X.
                                                                                                                                                                                                                                                                                                                                                                    Missing (14. /FTId=VSP_002673. /FTId=VSP_002673. / -> M (in dbSNP:2227329).
                                                                                                                                                                                                          <u>.</u>
                                                                                                                                                                                                        Score 884.5; |
Pred. No. 6.1e
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                 0-linked
                                                                                                                                                                                                                                                                                                                                                                                                                                          Granulocyte colony-stimulating
                                                                                                                                                                                                                                                                                                                                                         FTId=VAR_013074.
                                                                                                                                                                                                                                                                                                                                                                /FTId=VAR_013073.
A -> T (in dbSNP:2227330)
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Polymorphism;
                                                                                                                                                                                                                                             421F635ECC776996 CRC64;
                                              194
                                                                                                                                                                                                                                                                                                                                                                                                       (in isoform
 precursor
          update)
                                                                                                                                                                                                                  6.1e-73;
                                              ₽
                                                                                                                                                                                                                          DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Signal
                                                                                                                                                                                                         0,
(G-CSF)
                                                                                                                                                                                                                                                                                                                                                                                                       Short)
                                                                                                                                                                                                                          Length
                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                (By
 (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                similarity)
                                                                                                                                                                                                                           207;
                                                                                                                                                                                                                                                                                                                                                                                                                                            factor
                                                                                                                                                                                                        Gaps
                                                                                                                                                 117
                                                                                                                                150
                                                                                                                                                                    90
                                                                                                                                                                                     57
```

```
RESULT 4
Q9GJU0
ID Q9GJU0
                                                                                                                                                                                                                                                                                                                  Query Match
Best Local S
Matches 141
                                                                                                                                                                                                                                                                                                                                                                                            DISULFID
DISULFID
CARBOHYD
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SMART; SMOULZS; LEU, LEUKIN 6; 1.
PROSITE; PS00254; INTERLEUKIN 6; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; Y08558; CAA69853.1; -. PIR; T09255; T09255.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ProDom; PD008388; GCSF_MGF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRINTS; PR00433; IL6GCSFMGF.
PRINTS; PR00434; INTERLEUKIN6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Name=CSF3;
Felis silvestris catus (Cat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eukaryota; Metazoa; Carnivora; Fissipedia; Felidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NON TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF00489; IL6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 entities requires a license agreement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Dunham S.P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=European shorthair; TISSUE=Lung;
MEDLINE=21389237; PubMed=11497496; DOI=10.1006/cyto.2001.0910;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              interPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HSSP; P09919; 1RHG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cytokine 14:347-351(2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    feline granulocyte colony-stimulating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Isolation, nucleotide sequence and expression of feline granulocyte colony-stimulating factor.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SIMILARITY: Belongs to the IL-6 superfamily.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FUNCTION: Granulocyte/macrophage colony-stimulating factors are cytokines that act in hematopoiesis by controlling the production, differentiation, and function of 2 related white cell populations of the blood, the granulocytes and the monocytes-macrophages. This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUBCELLULAR LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUBUNIT: Monomer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PTM: O-glycosylated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CSF induces granulocytes (By similarity).
                                                                                             141
                                                                                                                                121
                                                                                                                                                                    81
                                                                                                                                                                                                         61
                                                                                                                                                                                                                                            21
                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                         MEDVGMAPAVPPTQGTMPTFTSAFQRRAGGTLVASNLQSFLEVAYRALRHFTKP
                                                                                                                                                                 LSSCSSQALQLTGCLRQLHSGLFLYQGLLQALAGISPELAPTLDMLQLDITDFAINIWQQ
                                                                                                                                                                                                    LSSCPSQALQLAGCLSQLHSGLFLYQGLLQALEGISPELGFTLDTLQLDVADFATTIWQQ
                                                                                                                                                                                                                                                                             TPLGPASSLPQSFLLKCLEQVRKIQGDGAALQEKLCATYKLCHPEELVLLGHSLGIPWAP
                                                                                                                          MEELGMAPALQPTQGAMPAFASAFQRRAGGVLVASHLQSFLEVSYRVLRHLAQP
                                                                                                                                                                                                                                        TPLGPTSSLPQSFLLKCLEQVRKVQADGTALQERLCAAHKLCHPEELVLLGHALGIPQAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IPR009079; 4 helix cytokine.
IPR003629; GCSF MGF.
IPR003573; IL6 MGF GCSF.
IPR003574; Interleukin_6.
                                                                                                                                                                                                                                                                                                                                                                                        153
194
PRELIMINARY;
                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Onions D.E.;
                                                                                                                                                                                                                                                                                                                                                                                              AA,
                                                                                                                                                                                                                                                                                                                                                                                              153
21154
                                                                                                                                                                                                                                                                                                                                                                                                                                   194
194
62
94
                                                                                                                                                                                                                                                                                                                                      83.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (By similarity)
                                                                                                                                                                                                                                                                                                                                                                                            MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Secreted.
                                                                                                                                                                                                                                                                                                                                      Score 744;
Pred. No. 4.
                                                                                                                                                                                                                                                                                                                                                                                                               O-linked (GalNAc.
                                                                                                                                                                                                                                                                                                                                                                                                                             Granulocyte colony-stimulating factor.
By similarity.
By similarity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Potential.
                                                                                                                                                                                                                                                                                                                                                                                            F72B7AB3DAE7385E
                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                There are no rest
                                                                                                                                                                                                                                                                                                                                      .2e-60;
                                                                                                                                                                                                                                                                                                                                                       DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Usage
                                                                                                                                                                                                                                                                                                                                                                                            CRC64;
                                                                                                                                                                                                                                                                                                                                                     Length 194;
                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       a cDNA encoding
                                                                                                                                                                                                                                                                                                                                                                                                         (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 λģ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Euteleostomi; Felis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   restrictions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          a collaboration
                                                                                                                                                                                                                                                                                                                  <u>,,</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         outstation
                                                                                           194
                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ģ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     엵
                                                                                                                                                                                                    120
                                                                                                                                                                   140
                                                                                                                                                                                                                                          80
                                                                                                                                                                                                                                                                             60
                                                                                                                                                                                                                                                                                                                  . 0
```

POOCE REPRESENTATION OF THE PROPERTY OF THE PR

Ś В Ś 묽 S

195

B

```
RESULT

ID PT

AC QC

A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    á
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         문
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SO THE CONTRACT OF THE CONTRAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local S
Matches 141
                                                                                                                                                                                                                                                                                                                                                                                                    CSF3_SHEEP
Q28746;
30-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SHEEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Signal.
SIGNAL
                                                                                                                                   Eukaryota; Metazoa;
Mammalia; Eutheria;
Caprinae; Ovis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR009079; 4 helix cytokine. InterPro; IPR003629; GCSF MGF. InterPro; IPR003573; IL6_MGF_GCSF. InterPro; IPR003574; Interleukin_6. Pfam; PF00489; IL6; 1.
                                                                                                                                                                                                                                                                                                                                     30-MAY-2000
05-JUL-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Molecular cloning and expression of the granulocyte colony-stimulating factor."; Gene 274:263-269(2001).
          MEDLINE=95102116;
                                  SEQUENCE FROM N.A.
                                                                                             NCBI_TaxID=9940;
                                                                                                                                                                                                                                        Ovis aries (Sheep)
                                                                                                                                                                                                                                                                              Name=CSF3;
                                                                                                                                                                                                                                                                                                      Granulocyte colony-stimulating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE; PS00254; INTERLEUKIN_6; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ProDom; PD008388; GCSF_MGF; 1.
SMART; SM00126; IL6; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRINTS; PR00433; IL6GCSFMGF.
PRINTS; PR00434; INTERLEUKIN6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HSSP; P35834; 1BGE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AB042552; BAB17789.1; -. EMBL; AB042553; BAB17757.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Yamamoto A., Iwata A.,
Tsujimoto H., Hasegawa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Carnivora; Fissipedia; Felidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Felis silvestris catus (Cat).
Eukaryota; Metazoa; Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Name=G-CSF;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Granulocyte colony-stimulating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-MAR-2001
05-JUL-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=21531548; PubMed=11675019; Yamamoto A., Iwata A., Tuchiya K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GO:0005576; C:extracellular; IEA.
GO:0005125; F:cytokine activity; IEA.
GO:0005138; F:interleukin-6 receptor
GO:0006955; P:immune response; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          141;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121 MEELGMAPALQPTQGAMPAFASAFQRRAGGVLVASHLQSFLEVSYRVLRHLAQP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ш
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LSSCPSQALQLAGCLSQLHSGLFLYQGLLQALEGISPELGPTLDTLQLDVADFATTIWQQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TPLGPASSLPQSFLLKCLEQVRKIQGDGAALQEKLCATYKLCHPEELVLLGHSLGIPWAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDVGMAPAVPTTQGTMPTFTSAFQRRAGGTLVASNLQSFLEVAYRALRHFTKP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LSSCSSQALQLTGCLRQLHSGLFLYQGLLQALAGISPELAPTLDMLQLDITDFAINIWQQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TPLGPTSSLPQSFLLKCLEQVRKVQADGTALQERLCAAHKLCHPEELVLLGHALGIPQAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (TrEMBLrel. (TrEMBLrel. (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                  (Rel.
(Rel.
(Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hasegawa A., Ueda
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                     39,
44,
      PubMed=7528579;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22 I
21255 MW;
                                                                                                                                                                      Chordata; Craniata; Vertebrata;
Cetartiodactyla; Ruminantia; Pe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         83.0%;
                                                                                                                                                                                                                                                                                                   Last sequence up
Last annotation
imulating factor
                                                                                                                                                                                                                                                                                                                                                                                                           Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16, Created)16, Last sequence update)27, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 744; DB 2;
Pred. No. 4.2e-60;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Potential
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      factor precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          544C682909412FCF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                      e update)
ion update)
:or (G-CSF)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DOI=10.1016/S0378-1119(01)00575-3;
Katsumata A., Oishi K., Saito T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                binding; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cDNA encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 195;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                         Euteleostomi;
cora; Bovidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Euteleostomi, Felis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0
```

Canis familiaris (Dog). Canis familiaris (Dog). Eukaryota; Metazoa; Chordata; ( Mammalia; Eutheria; Carnivora;

Craniata; Vertebrata; ; Fissipedia; Canidae;

Euteleostomi; Canis.

Name=CSF3

sequence up annotation ating factor

update) (G-CSF)

update)

NCBI\_TaxID=9615;

MEDLINE=94076341; Lovejoy B., Cascic

Cascio

Ü

X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS)

PubMed=7504736;

```
RESULT
CSP3_CA
ID CS
AC P3
AC P3
DT 011
DT 011
DT 012
DB GE
CB
OS 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ś
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ś
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ś
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity Matches 143; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                      CSF3 CANFA
P35834;
01-JUN-1994
                                                                                                                                                                                                                                                                                                                                                                                    CANFA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DISULFID
CARBOHYD
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collable between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for commodified and this statement is not removed. Usage by and for commodified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -i-
                                                                                                                                                                                                                           01-JUN-1994 (Rel. 29, Last seq
25-OCT-2004 (Rel. 45, Last anno
Granulocyte colony-stimulating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SMART; SM00126; IL6; 1.

PROSTTE; PS00254; INTERLEUKIN 6; 1.
Cytokine; Glycoprotein; Growth fact
DISULFID 36 42 By sim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; L07939; AAA68006.1; --
PIR; T10268; T10268.
HSSP; P09919; 1RHG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         O'Brien P.M., "Cloning and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR009079; 4 helix cytokine
InterPro; IPR003629; GCSF MGF.
InterPro; IPR003573; IL6 MGF GCSF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      factor cDNA.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF00489;
PRINTS; PR0043;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Seq. 4:339-342(1994).
FUNCTION: Granulocyte/macrophage colony-stimulating factors are cytokines that act in hematopoissis by controlling the product differentiation, and function of 2 related white cell population of the blood, the granulocytes and the monocytes-macrophages.

CSF induces granulocytes (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PTM: O-glycosylated (By similarity). SIMILARITY: Belongs to the IL-6 superfamily.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUBCELLULAR LOCATION: Secreted.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ۱...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PR00433; IL6GCSFMGF.
PD008388; GCSF_MGF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEELGMAPALQPTQGAMPAFASAFQRRAGGVLVASHLQSFLEVSYRVLRHLAQP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TPLGPASSLPQSFLLKCLEQVRKIQGDGAALQEK1.CATYKLCHPEELVLLGHSLGIPWAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LSSCPSQALQLAGCLSQLHSGLFLYQGLLQALEGISPELGPTLDTLQLDVADFATTIWQQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              and sequencing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TPLGPARSLPQSFLLKCLEQVRKIQADGAELQERLCATHKLCHPEELVLLGHSLGIPQAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LSSCSSQSLQLTSCLDQLHGGLFLYQGLLQALAGISPELAPTLDTLQLD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       64
133
174 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IPR009079; 4
                                                                                                                                                                                                                                                      (Rel.
(Rel.
(Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Seow H.F.,
                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                      29,
45,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18806 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            82.4%;
                                                                                                                                                                                                                                                                                                            Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              , Rothel J.S., Wood P.R.; of an ovine granulocyte colony-stimulating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       By similarity.
By similarity.
O-linked (GalNAc. . .) (B
A5AA8F8D23ACD1E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 738; DB 1; Pred. No. 1.3e-59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  factor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                               175
                                                                                                                                                                                                                                                                                                                                                               8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 174;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .) (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   actors are
ne production,
populations
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VTDFATNIWLQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      60
```

```
RESULT 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local S
Matches 140
                                                        CSF3_BOVIN STANDARD; PRT; 195 AA.
P35833; Q9TV89;
01-JUN-1994 (Rel. 29, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
Granulocyte colony-stimulating factor precursor
                                                                                                                                                                                                                                                                                                                                                                                                                   TURN
HELIX
TURN
STRAND
             Name=CSF3; Synonyms=GCSF;
Bos taurus (Bovine).
Eukaryota; Metazoa; Chord
Mammalia; Eutheria; Cetar
                                                                                                                                             BOVIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TURN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAND
HELIX
HELIX
Bovinae; Bos
                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TURN
HELIX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TURN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Crystal structure of canine and bovine granulocyte-colony stimulating factor (G-CSF).";
J. Mol. Biol. 234:640-653(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HELIX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PDB; 1BGD; X-ray; @=1-175.
PDB; 1BGE; X-ray; A/B=1-175.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HELIX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PS00254; INTERLEUKIN_6; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ProDom; PD008388;
SMART; SM00126; I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRINTS; PR00433; IL6GCSFMGF.
ProDom; PD008388; GCSF_MGF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF00489;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         D-structure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      interPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SIMILARITY: Belongs to the IL-6 superfamily
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PTM: O-glycosylated.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUBUNIT: Monomer.
SUBCELLULAR LOCATION: Secreted.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FUNCTION: Granulocyte/macrophage colony-stimulating facytokines that act in hematopoiesis by controlling the differentiation, and function of 2 related white cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CSF induces granulocytes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      of the blood, the
                                                                                                                                                                                                123
                                                                                                                                                                                                                       122
                                                                                                                                                                                                                                                                                                                                                       140;
                                                                                                                                                                                                                                                63
                                                                                                                                                                                                                                                                          62
                                                                                                                                                                                                                                                                                                     w
                                                                                                                                                                                                                                                                                                                             N
                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                SSCSSQALQLMGCLRQLHSGLFLYQGLLQALAGISPELAPTLDTLQLDTTDFAINIWQQM
                                                                                                                                                                                                                                                              SSCPSQALQLAGCLSQLHSGLFLYQGLLQALEGISPELGPTLDTLQLDVADFATTIWQQM
                                                                                                                                                                                               EDLGMAPAVPPTQGTMPAFTSAFQRRAGGVLVASNLQSFLELAYRALRHFAKP
                                                                                                                                                                                                                EELGMAPALQPTQGAMPAFASAFQRRAGGVLVASHLQSFLEVSYRVLRHLAQP 174
                                                                                                                                                                                                                                                                                                  PLGPTGPLPQSFLLKCLEQMRKVQADGTALQETLCATHQLCHPEELVLLGHALGIPQPPL
                                                                                                                                                                                                                                                                                                                             PLGPASSIPQSFILKCLEQVRKIQGDGAALQEKICATYKICHPEELVLLGHSIGIPWAPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IPR009079; 4 helix cytokine. IPR003629; GCSF_MGF. IPR003573; IL6_MGF_GCSF.
                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cytokine; Glycoprotein; Growth factor
                                                                                                                                                                                                                                                                                                                                                                                                       AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    116;
                                                                                                                                                                                                                                                                                                                                                                                                                                  39
55
69
92
92
100
125
171
171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   75
134
              Cetartiodactyla;
                         Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                       18858 MW;
                                                                                                                                                                                                                                                                                                                                                                   80.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      granulocytes and the monocytes-macrophages.
                                                                                                                                                                                                                                                                                                                                                Pred. No. 3.10
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                             Score 734;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     O-linked (GalNAc. .
              Craniata; Vertebrata; Euteleostomi;
actyla; Ruminantia; Pecora; Bovidae;
                                                                                                                                                                                                                                                                                                                                                                                                        28C26B24990C6DB3
                                                                                                                                                                                                                                                                                                                                                     3.1e-59;
ches 22;
                                                                                                                                                                                                                                                                                                                                                                                DB 1;
                                                                                                                                                                                                                                                                                                                                                                               Length 175;
                                                                (G-CSF).
                                                                                                                                                                                                                                                                                                                                                                                                        CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .) (By similarity)
                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    the production, ell populations acrophages. This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           factors
                                                                                                                                                                                                                                                                                                                                                     0
                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          are
                                                                                                                                                                                                                                                122
                                                                                                                                                                                                                                                                          121
                                                                                                                                                                                                                                                                                                   62
                                                                                                                                                                                                                                                                                                                            61
                                                                                                                                                                                                                                                                                                                                                     0,
```

FT

SAFFFFF BROSSSS

밁 ş

S

61 22

LSSCPSQALQLAGCLSQLHSGLFLYQGLLQALEGISPELGPTLDTLQLDVADFATTIWQQ 120

TPLGPARSLPQSFLLKCLEQVRKIQADGAELQERLCAAHKLCHPEELMLLRHSJ TPLGPASSLPQSFLLKCLEQVRKIQGDGAALQEKLCATYKLCHPEELVLLGHSLGIPWAP

GIPQAP

81 60 δ 밁 Ś 밁 Ś

```
Query Match
Best Local S
Matches 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        [1]
SEQUENCE FROM N.A.
STRAIN=Holstein;
                                                                                                                                                                                                CARBOHYD
CONFLICT
                                                                                                                                                                                                                      CHAIN
DISULFID
DISULFID
                                                     TURN
TURN
TURN
TURN
HELIX
HELIX
                                                                                                                                           HELIX
TURN
                                                                                                                                HELIX
                                                                                                                                                                  TURN
                                                                                                                                                                                                                                                                                     ProDom; PD008388;
SMART; SM00126; II
                                                                                                                                                                                                                                                                                                                                                                                                                      between the Swiss Institute of Bioinformat
the European Bioinformatics Institute. The
use by non-profit institutions as long
modified and this statement is not removed.
                                           SEQUENCE
                                                                                                                                                                            HELIX
                                                                                                                                                                                     HELIX
                                                                                                                                                                                                                                                                                                                                                                EMBL; AF092533; AAD16102.1; -. PDB; 1BGC; X-ray; @=22-195.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                This
                                                                                                                                                                                                                                                       SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                 or send
                                                                                                                                                                                                                                                                                                                                                                                                            entities requires a license agreement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      factor (G-CSF).";
J. Mol. Biol. 234:640-653(1993).
                                                                                                                                                                                                                                                                 3D-structure;
                                                                                                                                                                                                                                                                            PROSITE; PS00254;
                                                                                                                                                                                                                                                                                                           PRINTS; PR00433; IL6GCSFMGF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lovejoy B., Cascio D., Eisenberg "Crystal structure of canine and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                X-RAY CRYSTALLOGRAPHY (1.7 ANGSTROMS)
WEDLINE=94076341; PubMed=7504736;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=94076341;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (SEP-1998) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Cloning, sequencing, and analysis of colony stimulating factor.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Heidari M., Kehrli M.E. Jr.;
                                                                                                                                                                                                                                                                                                                       efam; PF00489; IL6;
                                                                                                                                                                                                                                                                                                                                InterPro; IPR003573;
                                                                                                                                                                                                                                                                                                                                            nterPro;
                                                                                                                                                                                                                                                                                                                                                      interPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SIMILARITY: Belongs to the IL-6 superfamily.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUBUNIT: Monomer.
SUBCELLULAR LOCATION: Secreted.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               differentiation, and func
of the blood, the granulo
CSF induces granulocytes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FUNCTION: Granulocyte/macrophage colony-stimulating factors an cytokines that act in hematopoiesis by controlling the product differentiation, and function of 2 related white cell population the blood, the granulocytes and the monocytes-macrophages.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PTM: O-glycosylated.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                SWISS-PROT entry is copyright. It is produced through a collaboration
           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                      C; X-ray; @=zz-1ys.; IPR009079; 4 heli; IPR003629; GCSF W
                                           195
 Conservative
                                                                                                            22
857
93
93
32
70
70
70
70
83
                                                                                                                                                                                                                                                                 Cytokine;
                                          Å,
                                                                                                                                                                                                                                                                                      IL6;
                                                                                                                                                                                                                                                     INTERLEUKIN_6; 1.
okine; Glycoprotein; Growth factor; Signal
21
    Potential.
                                                                                                                                                                                                                                                                                              GCSF_MGF; 1.
                                                                           76
85
89
112
115
120
                                           21431
         81.1%;
                                                                                                                                                                                                                                                                                                                               IL6_MGF_GCSF.
                                                                                                                                                                                                                                                                                                                                             helix cytokine
                                          MW;
          Score 727;
Pred. No. 1.
                                                                                                                                                                                                O-linked
TS -> RG
                                                                                                                                                                                                                                           Granulocyte colony-stimulating
                                          8C06119E4ADFBA73 CRC64;
 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bioinformatics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           D.;
bovine
                                                                                                                                                                                                (GalNAc. .
(in Ref. 2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cDNA encoding bovine
                                                                                                                                                                                                                                                                                                                                                                                                            (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           granulocyte-colony stimulating
          DB 1;
.5e-58;
                                                                                                                                                                                                                                                                                                                                                                                                                                          There are no
                                                                                                                                                                                                                                                                                                                                                                                                                                 as
                                                                                                                                                                                                                                                                                                                                                                                                                        Usage
                                                                                                                                                                                                                                                                                                                                                                                                                                its content
                   Length ·195
                                                                                                                                                                                                                                                                                                                                                                                                                                                      and the
 Indels
                                                                                                                                                                                                           (By similarity)
                                                                                                                                                                                                                                                                                                                                                                                                                                          restrictions
                                                                                                                                                                                                                                                                                                                                                                                                                        and
                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ne production,
| populations
|rophages. This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       granulocyte
0
                                                                                                                                                                                                                                            factor.
                                                                                                                                                                                                                                                                                                                                                                                                                        for
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                        commercia
                                                                                                                                                                                                                                                                                                                                                                                                                                  ខ្ល
                                                                                                                                                                                                                                                                                                                                                                                                                                             8
0
```

δ

```
RESULT 8
CSP3 LPIG
ID CSP3
AC CO28
AC 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ś
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     문
Query Match
Best Local
                                                                              CARBOHYD
CONFLICT
                                                                                                                 DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                               EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gloster S.E., Sandeman R.M., "Cloning of a cDNA and gene stimulating factor."; submitted (SEP-1997) to the
                                                                                                                                                                                                                                                                                                                                                                          EMBL; U68482; AAB70701.1; -. EMBL; U68481; AAB70700.1; -. HSSP; P09919; 1RHG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30-MAY-2000 (Rel. 39, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Granulocyte colony-stimulating factor precursor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  002837; 019180;
15-JUL-1998 (Re
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CSF3
                                                           SEQUENCE
                                                                                                                                                                           SIGNAL
                                                                                                                                                                                              Cytokine;
                                                                                                                                                                                                                                         SMART;
                                                                                                                                                                                                                                                                        PRINTS; PRO0433; IL6GCSFMGF
                                                                                                                                                                                                                                                                                                           InterPro; IPR009079; 4 helix cytokine
InterPro; IPR003629; GCSF MGF.
InterPro; IPR003573; IL6 MGF GCSF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             or send
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (JAN-1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sus scrofa (Pig).
                                                                                                                                                                                                                PROSITE;
                                                                                                                                                                                                                                                          ProDom; PD008388;
                                                                                                                                                                                                                                                                                               Pfam; PF00489; IL6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    modified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE=Liver;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Kulmburg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=9823;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Name=CSF3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              European Bioinformatics Institute. The by non-profit institutions as long ified and this statement is not removed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PTM: O-glycosylated (By similarity). SIMILARITY: Belongs to the IL-6 superfamily.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUBUNIT: MODOMER.
SUBCELLULAR LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   differentiation, of the blood, the CSF induces gran
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FUNCTION: Granulocyte/macrophage colony-stimulating cytokines that act in hematopoiesis by controlling t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                121
                                                                                                                                                                                                                                                                                                                                                                                                                                 Y10494;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       82
                                                                                                                                                                                                                                     SM00126;
  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             an email to license@isb-sib.ch)
                                                                                                                                                                                                                   PS00254;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       induces granulocytes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ס.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           requires a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEELGMAPALOPTQGAMPAFASAFQRRAGGVLVASHLQSFLEVSYRVLRHLAQP 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LSSCSSQSLQLTSCLNQLHGGLFLYQGLLQALAGISPELAPTLDTLQLDVTDFATNIWLQ
                                                                                                                                                                                              Glycoprotein;
                                                                              22
57
85
154
123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (Rel. 36,
                                                                                                                                                                                                                                                                                                                                                                                                                                      CAA71518.1; -.
                                                         ₽,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                     IL6;
                                                                                                                                                                                                                                                    GCSF_MGF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ..., and runction of 2 related white cell populations the granulocytes and the monocytes-macrophages. This ranulocytes (By similarity)
                                                                                                                                                                                                                INTERLEUKIN
                                                                            21
195
63
95
154
123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chordata; Craniata; Vertebrata; Cetartiodactyla; Suina; Suidae;
                                                           21214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  License
78.3%;
79.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ő
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Created)
                                                                                                                                                                             Growth fa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            the
                                                           M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Secreted
                                                                    agreement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Strom A.D.G.;
encoding porci
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL/GenBank/DDBJ databases
  Score
Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                           84787F20DB0AEA1C
                                                                                                                                                                                              factor; Signal.
702; DB 1;
No. 3e-56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           porcine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (See
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   There are no rest
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               http://www.isb-sib.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Usage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               granulocyte-colony
                    Length 195;
                                                           CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (G-CSF)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Euteleostomi;
Sus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         restrictions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 the production,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     factors
                                                                                                 similarity)
                                                                                                                                                           factor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ġ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           141
```

```
RESULT 9
CSF3_MOUSE
Ś
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              문
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                           This SWISS-PROT entry is copyright. It is provent the EMBL our the Swiss Institute of Bioinformatics and the EMBL our the Swiss Institute. There are no restrictions in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              עס-טער (Rel. 44, Last annotation update) Granulocyte colony-stimulating factor precursor (G-CSF).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CSF3_MO
P09920;
                                                 EMBL; M13926; AAA37672.1; EMBL; X05402; CAA28986.1:
                                                                                                  the European Bioinformatics Institute. There use by non-profit institutions as long as modified and this statement is not removed. Use not the statement is not removed.
                                                                                                                                                                                            -!- SUBCELLULAR LOCATION: Secreted.
-!- PTM: O-glycosylated (By similarity).
-!- SIMILARITY: Belongs to the IL-6 superfamily.
                                                                                                                                                                                                                                                                                                                     Biol
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDILINE=87017003; PubMed=3489940;
Tsuchiya M., Asano S., Kaziro Y., Nagata
"Isolation and characterization of the cD
colony-stimulating factor.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Name=Csf3; Synonyms=Csfg;
Mus musculus (Mouse).
            PIR; A29536; A26496.
HSSP; P09919; 1RHG.
MGD; MGI:1339751; Cs
                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=87190474; PubMed=3494605;
Tsuchiya M., Kaziro Y., Nagata S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-MAR-1989
                                                                                        or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                         Simpson R.J.,
                                                                                                                                                                                                                                                                                                                                                                       PubMed=3501294;
                                                                                                                                                                                                                                                                                                                                                                                      PARTIAL SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                             stimulating factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-MAR-1989
                                                                                                                                                                                                                                                                                                                                  factor.
                                                                                                                                                                                                                                                                                                                                               'Structural studies
                                                                                                                                                                                                                                                                                                                                                                                                                                          "The chromosomal gene structure
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Proc. Natl. Acad. Sci. U.S.A.
                                                                                                                                                                                                                        SUBUNIT: Monomer.
SUBCELLULAR LOCATION:
                                                                                                                                                                                                                                                                                                         FUNCTION:
                                                                                                                                                                                                                                                     CSF
                                                                                                                                                                                                                                                               of the blood, the granulocytes
                                                                                                                                                                                                                                                                              differentiation, and function of
                                                                                                                                                                                                                                                                                         cytokines that act
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    137;
                                                                                                                                                                                                                                                                                                                     Chem.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N
                                                                                                                                                                                                                                                                                                                                                                                                                 Biochem. 165:7-12(1987)
                                                                                                                                                                                                                                                  induces granulocytes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EELGWAPALQPTQGAMPAFASAFQRRAGGVLVASHLQSFLEVSYRVLRHLAQP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SSCPSQALQLAGCLSQLHSGLFLYQGLLQALEGISPELGPTLDTLQLDVADFATTIWQQM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PLSPASSLPQSFILKCLEQVRKIQADGAELQERLCATHKLCHPQELVLLGHSLGLPQASL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PLGPASSLPQSFLLKCLEQVRKIQGDGAALQEKLCATYKLCHPEELVLLGHSLGIPWAPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EDLRMAPASLPTQGTVPTFTSAFQRRAGGVLVVSQLQSFLELAYRVLRYLAEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SSCSSQALQLTGCLNQLHGGLVLYQGLLQALAGISPELAPALDILQLDVTDLATNIWLQM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (Rel.
                                                                                                                                                                                                                                                                                                                    Hoppe-Seyler 368:1327-1331(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                             Granulocyte/macrophage colony-stimulating fa
that act in hematopoiesis by controlling the
iation, and function of 2 related white cell
                                                                                                                                                                                                                                                                                                                                                            Nice E.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10, Last sequence up
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10, Created)
                                                                                                                                                                                                                                                                                                                                               엺
                                                                                                                                                                                                                                                                                                                                               the
                                                                                                                                                                                                                                                                                                                                           Nicola N.A.;
he murine granulocyte
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            83:7633-7637(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                            for
                                                                                                                                                                                                                                                                  and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 update)
                                                                                                                                                                                                                                                                                                                                                                                                                                          murine granulocyte colony
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         208
                                                                                                                                                                                                                                                                  the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   :
:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A
                                                                                                      http://www.
                                                                                                                                                                                                                                                                  monocytes-macrophages.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       for murine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    25;
                                                                                                                                                                                                                                                                                                                                               colony-stimulating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                        isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                            the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       granulocyte
                                                                                                                                                                                                                                                                                                         factors
                                                                                                                                                                                                                                                                   populations
ophages. This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      <u>.</u>.
                                                                                                                     for
                                                                                                                                                                       collaboration
                                                                                                                                                           outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                     commercia.
                                                                                                                                             9
                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0
```

interPro;

IPR009079;

4\_helix\_cytokine.

Csf3

```
Ś
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 127; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 129; Conserv
                                                                            PRINTS; PRO0433; ILGGCSFMGF; 1.
ProDom; PD008388; GCSF MGF; 1.
SMART; SM00126; ILG; 1.
PROSITE; PS00254; INTERLEUKIN PROPINTS 
                                                                                                                                                                                                                                                             HSSP; P09919; 1RHG.
GO; GO:00055125; F:cytokine activity; IEA.
GO; GO:0005125; F:cytokine activity; IEA.
GO; GO:0008083; F:growth factor activity;
GO; GO:0006955; P:immune response; IEA.
                                                                                                                                                                                                                                                                                                                                                                  Gene 175:101-104(1996).
EMBL; U37101; AAC52915.1; -.
PIR; UC5043; UC5043
                                                                                                                                                                              InterPro; IPR009079; 4 helix cytokine.
InterPro; IPR003629; GCSF MGF.
InterPro; IPR003573; IL6 MGF GCSF.
Pfam; PF00489; IL6; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Granulocyte colony stimulating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      P97712;
01-MAY-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DISULFID
DISULFID
CARBOHYD
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Signal.
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                    stimulating factor.",
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Han S.W., Ramesh N., Osborne W.R.; "Cloning and expression of the cDNA encoding rat granulocyte colony-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   P97712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=97074656;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRINTS; PR00433; IL6GCSFMGF.
ProDom; PD004358; GCSF MGF; 1.
ProDom; PD004356; Interleukin_6;
SMART; SM00126; IL6; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR003629;
InterPro; IPR003573;
Pfam; PF00489; IL6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cytokine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE; PS00254;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ω
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NLGVAPTVQPTQSAMPAFTSAFQRRAGGVLAISYLQGFLETARLALHHLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ELGMAPALOPTOGAMPAFASAFORRAGGVLVASHLQSFLEVSYRVLRHLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SCPSQALQLAGCLSQLHSGLFLYQGLLQALEGISPELGPTLDTLQLDVADFATTIWQQME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LPSLPLPRSFLLKSLEQVRKIQASGSVLLEQLCATYKLCHPEELVLLGHSLGIPKASLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LGPASSLPQSFLLKCLEQVRKIQGDGAALQEKLCATYKLCHPEELVLLGHSLGIPWAPLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GCSSQALQQTQCLSQLHSGLCLYQGLLQALSGISPALAPTLDLLQLDVANFATTIWQQME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             169
208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30
208
78
110
169
22421
                                                                                 INTERLEUKIN 6; 1.
; 23659 MW; 29BB88B17B684C55 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PubMed=8917083; DOI=10.1016/0378-1119(96)00131-X;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INTERLEUKIN_6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chordata;
Rodentia;
                   70.8%;
73.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GCSF_MGF.
IL6_MGF_GCSF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   71.5%;
75.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sequencing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ₹
:
Score 634; DB
Pred. No. 5.6e
10; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Last sequence update)
Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 641; DB
Pred. No. 1.2e
9; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Granulocyte of By similarity By similarity O-linked (Galor)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Craniata; Ver
Sciurognathi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          factor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 p similarity.
p similarity.
p similarity.
placed (GalNAc. . .) (By similarity).
OBF3622135C906DB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Glycoprotein;
                 5.6e-50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Vertebrata; |
thi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 1; I
1.2e-50;
nes 32;
                                          DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ₽
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              colony-stimulating factor
                                                                                                                                                                                                                                                                                         IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           update)
                                      Length 214;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 208;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Growth factor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Buteleostomi;
; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0
```

Conservative

10;

35;

Indels

0

0

```
RESULT 12

MGF_CHICK STANDARD; PR

ID MGF_CHICK STANDARD; PR

AC P13854;

DT 01-JAN-1990 (Rel. 13, Created)

DT 01-JAN-1990 (Rel. 13, Last seque

DT 28-F2B-2003 (Rel. 41, Last annot

DE Myelomonocytic growth factor pre

OS Gallus gallus (Chicken).
                                                                                                                                                                                                                                                                                                                                   Ś
                                                                                                                                                                                                                                                                                                                                                                                          밁
                                                                                                                                                                                                                                                                                                                                                                                                                                    S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        맑
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A ID A COCC OF THE COCC OF THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT
Q8MKE0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ś
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  á
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ś
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local S
Matches 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SMART; SM00126; IL6; 1-
PROSITE; PS00254; INTERLEUKIN_6;
SEQUENCE 127 AA; 13657 MW; 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HSSP; P35833; IBGC.
GO; GO:0005576; C:extracellular; IEA.
GO; GO:0005125; F:cytokine activity; IEA.
GO; GO:0008083; F:growth factor activity;
GO; GO:0006955; P:immune response; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Noronha L.E., Takafu
Submitted (APR-2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRINTS; PR00433; IL6GCSFMGF.
ProDom; PD008388; GCSF_MGF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Name=G-CSF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Granulocyte
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q8MKE0;
01-OCT-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF00489; IL6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR009079; 4 helix cytokine.
InterPro; IPR003629; GCSF MGF.
InterPro; IPR003573; IL6 MGF GCSF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Equus caballus (Horse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-OCT-2002
01-MAR-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q8MKE0
                                                                                                                                                                                                                                                                                      121
                                                                                                                                                                                                                                                                                                                                        168
                                                                                                                                                                                                                                                                                                                                                                                                                                         108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            101;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   123
                                                                                                                                                                                                                                                                                                                                                                                       61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AF503365; AAM34205.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                      LRYLAEP 127
                                                                                                                                                                                                                                                                                                                                   LRHLAQP 174
                                                                                                                                                                                                                                                                                                                                                                                     LDVTDFATNIWQQMEDLGVAPVVQPTHGPMPTFASAFQRRAGGVLVASNLQRFLELAYRG
                                                                                                                                                                                                                                                                                                                                                                                                               LDVADFATTIWQQMEELGMAPALQPTQGAMPAFASAFQRRAGGYLVASHLQSFLEVSYRV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ELGMAPALQPTQGAMPAFASAFQRRAGGVLVASHLQSFLEVSYRVLRHLAQP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LPPSLPLPRSFLLKSLEQVRKIQARNTELLEQLCATYKLCHPEBLVLFGHSLGIPKASLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SLGVAPTVQPTQSTMPIFTSAFQRRAGGVLVTSYLQSFLETAHHALHHLPRP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SCPSQALQLAGCLSQLHSGLFLYQGLLQALEGISPELGFTLDTLQLDVADFATTIWQQME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LGPASSLPQSFLLKCLEQVRKIQGDGAALQEKLCATYKLCHPEELVLLGHSLGIPWAPLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SCSSQALQQTKCLSQLHSGLFLYQGLLQALAGISSELAPTLDMLHLDVDNFATTIWQQME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (Trembirel. 22, Created)
(Trembirel. 22, Last sequence update)
(Trembirel. 26; Last annotation updat colony-stimulating factor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Takafuji V.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chordata; Craniata; Vertebrata; Perissodactyla; Equidae; Equus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               57.0%;
79.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chordata;
                                                    Last sequence update)
Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 511; DB
Pred. No. 5.9e
9; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         F_GCSF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sharova L.V., Crisman M.V., EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; 1.
25559C2569802077
                                                                                                                                                        201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 2;
.9e-39;
                                                                                                                                                        A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 127;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Howard R.D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                     120
                                                                                                                                                                                                                                                                                                                                                                                                                                    167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        62
```

```
Matches
                                                                                                                                                                                                                                          Query Match
Best Local
                                                                                                                                                                                                                                                                                                                          DISULFID
DISULFID
CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       wausepohl H., Pan Y.-C.E., Smart J., Hayman M., Graf T.;
"Molecular cloning of the chicken myelomonocytic growth factor (cMGF)
reveals relationship to interleukin 6 and granulocyte colony
stimulating factor.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             [1]
SEQUENCE FROM N.A.
MEDLINE=89231616; PubMed=2785450;
Namm K., Sterneck E., F
Smart
                                                                                                                                                                                                                                                                                                                                                                                                                             Glycoprotein;
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ProDom; PD008388; GCSF_MGF; 1.
ProDom; PD004356; Interleukin_6; 1.
SMART; SM00126; IL6; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; M85034; AAA48694.1; -.
EMBL; X14477; CAA32639.1; -.
PIR; A42247; A42247.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   the European Bioinformatics Institute. There are no restriuse by non-profit institutions as long as its content imodified and this statement is not removed. Usage by and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=92195319; PubMed=1549124;
Sterneck E., Blattner C., Graf T., Leutz A.;
"Structure of the chicken myelomonocytic gro
                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE; PS00254; INTERLEUKIN 6; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          protein kinases."
Mol. Cell. Biol. 1
                                                                                                                                                                                                                                                                                                                                                                                                            CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRINTS; PR00433; IL6GCSFMGF.
PRINTS; PR00434; INTERLEUKIN6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       specific activation of its promoter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR009079; 4 helix cytokine.
InterPro; IPR003629; GCSF MGF.
InterPro; IPR003573; IL6 MGF_CCSF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SSP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  entities
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBO J. 8:175-181(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=9031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Archosauria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                nterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               tities requires a license agreement (S send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FUNCTION: Hematopoietic growth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SIMILARITY: Belongs to the IL-6 superfamily.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUBCELLULAR LOCATION: Secreted.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  proliferation and colony formation cells of the myeloid lineage.
                     131
                                                                                                                                           36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PF00489; IL6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              P09919; 1RHC
                                                             96
                                                                                                   71
                                                                                                                                                                                                                       67;
                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                   QSFLLKCLEQVRKIQGDGAALQBKLCATYKLCHPEELVLLGHSLGIPWAPLSSCPSQALQ 70
QPTQ--GAMPAFASAFQRRAGGVLVASHLQSFLEVSYRVLRHLAQ
                                                             AEVCFTQIRAGLHAYHDSLGAVLRLLPNHTTLVETLQLDAANLSSNIQQQMEDLGLDTVT 155
                                                                                                 LAGCLSQLHSGLFLYQGLIQALEGISPELGPTLDTLQLDVADFATTIWQQWEELGWAPAL 130
                                                                                                                                           QLFLHKNLEFTRKIRGDVAALQRAVCDTFQLCTEEELQLVQPDPHLVQAPLDQCHKRGFQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IPR003574;
                                                                                                                                                                                                                                                                                                       201 AA;
                                                                                                                                                                                                                                                                                                                                             24
61
89
123
                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12:1728-1735 (1992)
                                                                                                                                                                                                                                                                                                                                           201
67
99
123
                                                                                                                                                                                                                                        33.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Interleukin_6.
                                                                                                                                                                                                                                                                                                         M₩;
                                                                                                                                                                                                                       28;
                                                                                                                                                                                                                                          Score 304; DB 1; Length 201; Pred. No. 9.1e-20;
                                                                                                                                                                                                                                                                                                                      Myelomonocytic growth factor.
By similarity.
By similarity.
N-linked (GleNAc. . .) (Poten
N-linked (GleNAc. . .) (Poten
                                                                                                                                                                                                                                                                                                       240A8DD21B4244E6
                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     factor that stimulates the 
cion of normal and transform
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ij
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ic growth avian mye
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                       68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       wth factor gene myelomonocytic
                                                                                                                                                                                                                                                                                                         CRC64;
                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                              (Potential)
                                                                                                                                                                                                                                                                                                                                                 (Potential)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       transformed
                                                                                                                                                                                                                       2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   collaboration
                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            commercia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           avian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ã,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8
                                                                                                                                           95
```

음 성 음 성

```
Ś
                                         문
                                                          S
                                                                                  문
                                                                                                     Ś
                                                                                                                             밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               밁
밁
                                                                                                                                             Ś
                                                                                                                                                                       Matches
                                                                                                                                                                                Query Match
Best Local (
                                                                                                                                                                                                                CHAIN
SEQUENCE
                                                                                                                                                                                                                                     Signal
SIGNAL
                                                                                                                                                                                                                                                                   PRINTS; PRO0433; IL6GCSFMGF.
PRINTS; PR00434; INTERLEUKIN6.
ProDom; PD008388; GCSF_MGF; 1.
ProDom; PD004356; Interleukin_6; 1.
SMART; SM00126; IL6; 1.
                                                                                                                                                                                                                                                                                                                                    GO; GO:0005576; C:extracellular; IEA.
GO; GO:0005125; F:cycokine activity;
GO; GO:0005138; F:interleukin-f recep
GO; GO:0006955; P:immune response; IE
                                                                                                                                                                                                                                                                                                                                                                                        Submitted (JAN-2003) to the EMBL/GenBank/DDBJ EMBL; AJ309540; CAC40812.1; -. EMBL; AJ250838; CAC15566.2; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. Schneider K., Klaas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gallus gallus (Chicken).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  05-JUL-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-DEC-2001
01-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01X060
                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Salmonella
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Wigley P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Kaiser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (FEB-2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 090YI0;
                                                                                                                                                                                                                                                            PROSITE
                                                                                                                                                                                                                                                                                                                                                                                 HSSP;
                                                                                                                                                                                                                                                                                                                                                                                                                          Kaiser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Differential cytokine invasion by Salmonella"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=9031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Archosauria; Aves; Neognathae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Interleukin-6 precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        vicrobiology 146:3217-3226(2000)
                                         157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               156 LPAEQRSPPPTFSGPFQQQVGGFFILANFQRFLETAYRALRHLAR
                                                                                    101 NSMEMLVRNNLNLP----KVTEEDGCLLAGFDEEKCLTKLSSGLFAFQTYLEFIQETFDS
                                                                                                                                                                                                                                                                                                                           PF00489; IL6; 1.
                                                               99
                                                                                                        44
                                                                                                                             41
                                                                                                                                                                       46;
                                                                                                                                                                                 Similarity
                                                                                                                             LPPAAAVPLPAAADSSGEVGLEEEAGARRALLDCEPLARVLRDRAVQLQDEMCKKFTVCE
                                                                                                                                                LGPASSLP------OSFLLKCLEQVRKIQGDGAALQEKLCATYKLCH
IEKITMHLILRDFTSFMEKTVRAVRYL
                    ---VASHL-----QSFLEVSYRVLRHL
                                         EKONVESICYSTKHLAATIROMV---
                                                               LGPTLDTLQLDVADFATTIWQQMEELGMAPALQPTQGAMPAFASAFQRRAGGVL-----
                                                                                                      PEELVLLGHSLGIPWAPLSSCPSQALQLAG-----CLSQLHSGLFLYQGLLQALEGISPE
                                                                                                                                                                                                                 48
241 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gallinarum."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rothwell
                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (TrEMBLrel. (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                    F:cytokine activity; IEA.
F:interleukin-6 receptor
P:immune response; IEA.
                                                                                                                                                                                                                                                          INTERLEUKIN_6; 1.
                                                                                                                                                                                                                 241 r
26790 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ) R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ۲
                                                                                                                                                                                                                                      47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chordata;
                                                                                                                                                                                12.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            typhimurium,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        expression in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                19,
19,
27,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Galyov E.E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kaspers B., Staeheli the EMBL/GenBank/DDBJ
                                                                                                                                                                       35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Last annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Last
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Created)
                                                                                                                                                                                                                           Potential.
mature ChIL-6
                                                                                                                                                                               Score 111; DB 2
Pred. No. 0.053;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Craniata; Vertebrata; Euteleostomi; Galliformes; Phasianidae; Phasianidae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                  657F8049F25BD2F8 CRC64;
                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Salmonella
                                           ----INPDEVVIP--DSAAQKSLLANLKSDKDW
 233
                     171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         avian cells in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Barrow P.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            B
                                                                                                                                                                                                                                                                                                                                                binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              update)
                                                                                                                                                                                            2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ۳
:
                                                                                                                                                                       74;
                                                                                                                                                                                                                                                                                                                                                                                                                 databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              enteritidis
                                                                                                                                                                                           Length
                                                                                                                                                                                                                                                                                                                                                 IEA.
                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Burnside
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                response to
                                                                                                                                                                                             241;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               <u>.</u>
:
                                                                                                                                                                       52;
                                                                                                                                                                       Gaps
                                           206
                                                                152
                                                                                    156
                                                                                                         86
                                                                                                                               100
                                                                                                                                                    43
```

RESULT

14

```
RESULT 15
Q9XT80
                                                                                                                                                                                                                                                                                                                         Ś
                                                                                                                                                                                                                                                                                                                                                     밁
                                                                                                                                                                                                                                                                                                                                                                         S
                                                                                                                                                                                                                                                                                                                                                                                                   밁
                                                                                                                                                                                                                                                                                                                                                                                                                        S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AC OCC DIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local S
Matches 37
                                                                                                                             Interleukin 6.
Delphinapterus leucas (Beluga whale).
Delphinapterus leucas (Beluga whale).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Craniata; Odontoceti;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q8MJ75;
01-OCT-2002
01-OCT-2002
          Vet. Immunol. Immunopathol. EMBL; AF076643; AAD42929.1; HSSP; P05231; 1ALU.
                                  St-Laurent G., Archambault D., "Molecular cloning, phylogenetic analysis and expression whale (Delphinapterus leucas) interleukin 6.", Vet. Immunol. Immunopathol. 73:31-44(2000).
                                                                               SEQUENCE FROM N.A.
MEDLINE=20141864; PubMed=10678396; DOI=10.1016/S0165-2427(99)00150-6;
                                                                                                                                                                                                        01-NOV-1999
                                                                                                                                                                                                                    01-NOV-1999
                                                                                                                                                                                                                                COXTEO;
                                                                                                                                                                                                                                           Q9XT80
                                                                                                                   NCBI_TaxID=9749;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ProDom; PD004356; Interleukin_6; 1.
SMART; SM00126; IL6; 1.
PROSITE; PS00254; INTERLEUKIN_6; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
Lee D., Yoo H., Choi
Submitted (JUN-2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AF518322; AAM74938.1; HSSP; P05231; 1ALU.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota, Metazoa;
Mammalia; Eutheria;
NCBI_TaxID=9823;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRINTS; PR00433; IL6GCSFMGF.
PRINTS; PR00434; INTERLEUKIN6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-MAR-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q8MJ75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR003574;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  nterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            nterPro;
  GO:0005576;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GO:0005576; C:extracellular; IEA.
GO:0005125; F:cytokine activity;
GO:0005138; F:interleukin-6 recep
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GO:0006955;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 scrofa
                                                                                                                                                                                                                                                                                                     172
                                                                                                                                                                                                                                                                                                                             134
                                                                                                                                                                                                                                                                                                                                                     112
                                                                                                                                                                                                                                                                                                                                                                            75
                                                                                                                                                                                                                                                                                                                                                                                                   52
                                                                                                                                                                                                                                                                                                                                                                                                                          16
                                                                                                                                                                                                                                                                                                                                                                                                                                                  37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                    NAGLLDKLQSQNEWMKNTKIILILRSLEDFLQFSLRAIR 210
                                                                                                                                                                                                                                                                                                                         -QGAMPAFAS--AFQRRAGGVLVASHLQSFLEVSYRVLR 169
                                                                                                                                                                                                                                                                                                                                                                          LSQLHSGLFLYQGLLQALEGISPELGPTLDTLQLDVADFATTIWQQMEELGMAPALQPT-
                                                                                                                                                                                                                                                                                                                                                                                                 KTEELIKYILGKISAMREEMCEKYEKCENSKEVLAENNLNLPKMAEKDGCFQSGFNQETC
                                                                                                                                                                                                                                                                                                                                                                                                                         KCLEQVRKIQGDGAALQEKLCATYKLCHPEELVLLGHSLGIP-WAPLSSCPSQALQLAGC
                                                                                                                                                                                                                                                                                                                                                  LMRITTGLVEFQIYLDYLQKEYESNKGNVEAVQISTKALIQTLRQKGKNPDKATTPNPTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IPR009079; 4_helix_cytokine.
IPR003573; IL6_MGF_GCSF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (Pig)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (TrEMBLrel.) (TrEMBLrel.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  212 AA;
                                                                                                                                                                                          (TrEMBLrel. (TrEMBLrel.
                                                                                                                                                                                                                  (TrEMBLrel.
                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
C:extracellular; IEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      P:immune response;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      F:interleukin-6 receptor binding; IEA.
P:immune response; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INTERLEUKIN_6; 1.; 23881 MW; 1F54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chordata; Craniata; Vertebrata;
Cetartiodactyla; Suina; Suidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            12.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 I.;
to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Interleukin_6.
                                                                                                                                                                                          12,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22,
                                                                                                                                                                                                                                                                                                                                                                                                                                                 32;
                                                                                                                                                                                          Last
Last
                                                                                                                                                                                                                  Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Last
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 110.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1F540E7030BCFD77 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                          annotation
                                                                                                                                                                                                    sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                             No. 0.052;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IEA.
                                                                                                                                                                                                                                           208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      212
                                                                                                                                                                                                                                          8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ጅ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 2;
                                                                                                                                                                                         update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                  85;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Euteleostomi;
Sus.
                                                        of beluga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         212;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                          133
                                                                                                                                                                                                                                                                                                                                                                                                  111
                                                                                                                                                                                                                                                                                                                                                                                                                         74
                                                                                                                                                                                                                                                                                                                                                                                                                                                 ű
```

```
밁
                        S
                                                      밁
                                                                               δ
                                                                                                              밁
                                                                                                                                     Ś
                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 33; Conserv
                                                                                                                                                                                                                          PROSITE; PS00254; INTERLEUKIN_6; 1.
SEQUENCE 208 AA; 23456 MW; 81CC85C6E80389C4 CRC64;
                                                                                                                                                                                                                                                      ProDom; PD004356; Inter
SMART; SM00126; IL6; 1.
                                                                                                                                                                                                                                                                               PRINTS; PR00434; ILEGCSFMGF.
PRINTS; PR00434; INTERLEUKING.
                                                                                                                                                                                                                                                                                                                          InterPro; IPR009079; 4_helix_cytokine.
InterPro; IPR003573; IL6_MGF_GCSF.
InterPro; IPR003574; Interleukin_6.
                                                                                                                                                                                                                                                                                                              Pfam; PF00489; IL6;
                                                                                                                                                                                                                                                                                                                                                                      GO:0006955;
                                                                                                                                                                                                                                                                                                                                                                                                GO:0005125; F:cytokine
                                                      112
172
                           137
                                                                                  80
                                                                                                              52
                                                                                                                                        21
                                                    TGLLEYOIYLDYLQNEYEGDKGSIEAVQISIKALAQILRQKVKNPDEVTTPDPTTNASLM 171
                                                                                                            IKYILGKISAMRKEMCEKYDKCENSKEALAENNLNLPKMAEKDGCFQSGFNQETCLMRIT
                                                                                                                                        VRKIQGDGAALQEKLCATYKLCHPEELVLLGHSLGIP-WAPLSSCPSQALQLAGCLSQLH
NNLQSQNDDWMRNTKIILILRSLENFLQFSLRAVR
                       --MPAFASAFQRRAGGVLVASHLQSFLEVSYRVLR 169
                                                                                SGLFLYQGLLQALEGISPELGPTLDTLQLDVADFATTIWQQMEELGMAPALQPTQGA---
                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                      P:immune
                                                                                                                                                                                                                                                                  Interleukin_6;
                                                                                                                                                                                                                                                                                                                                                                                   nterleukin-6
                                                                                                                                                                                 12.1%; Score 108; DB 2 21.3%; Pred. No. 0.086;
                                                                                                                                                                                                                                                                                                                                                                   response;
                                                                                                                                                                    35;
                                                                                                                                                                                                                                                                                                                                                                                                activity;
                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                    vity; IEA.
  receptor binding; IEA.
se; IEA.
                                                                                                                                                                                              2
                                                                                                                                                                    81;
                                                                                                                                                                                             Length 208;
                                                                                                                                                                    Indels
                                                                                                                                                                    6,
                                                                                                                                                                  Gaps
                                                                                136
                                                                                                              111
                                                                                                                                        79
```

Search completed: July 9, 2005, 12:39:02 Job time : 110.682 secs

٠,

```
Result
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Minimum DB seq length: 0
Maximum DB seq length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Database :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                              Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                      110.5
108.5
106.5
101
                                                                                                                                                                                                                                                                                                                                            Score
                                                                                                                                                                                                                                                                                                                                           Match Length DB
                                                                                                                                                                                                                                                                                                                                                                                                                                   UniProt_03:*
1: uniprot_sprot:*
2: uniprot_trembl:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           July 9, 2005, 12:25:44; Search time 111.318 Seconds (without alignments) 805.025 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1612378 seqs, 512079187 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-10-751-242-2
901
   1 MTPLGPASSLPQSFLLKCLE.....
                                                                                                                                                                                                                                                                                                                      99.4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Copyright
   214
127
127
201
201
202
208
208
208
208
208
208
208
2189
2189
2189
2175
2175
2175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GenCore version 5.1.6 (c) 1993 - 2005 Compugen Ltd.
Q9KTL6
Q9NPP7
Q6NZ80
Q8MKE5
HMCU DROME
Q9A523
Q9A523
Q91019
Q8RJY3
Q9POS7
                                                                                                                                                                                                                                   CSF3_HUMAN
CSF3_FELCA
QOGATIO
CSF3_CANFA
CSF3_SHEEP
CSF3_BOVIN
CSF3_PIG
CSF3_MOUSE
                                                                                             IL6_FELCA
Q8D706
                                                                                                                              IL6_PIG
IL6_ORCOR
IL6_HORSE
Q6NZ82
                                                                                                                                                                    Q8MKE0
MGF_CHICK
Q90YI0
Q8MJ75
Q9XT80
                                                                                                                                                                                                                                                                                                                                            Ħ
                                                                                                                   29H2A5
                                                                                                                                                                                                                                                                                                                      28N4W3
                                                                                                                                                                                                                                                                                                                                                                          SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SHLOSFLEVSYRVLRHLAOP 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1612378
                                                                                                                                                                                                                                                                 Q8n4w3 homo sapien
P09919 homo sapien
O02708 felis silve
Q9gjuO felis silve
P35834 canis famil
Q28746 ovis aries
                     Q9a523
Q9i019
                                          Q6nz80
Q8mke5
P10180
                                                                                             P41683
Q8d706
                                                                                                                   Q6nz82
Q9h2a5
                                                                                                                                                                                           P13854
Q90yi0
                                                                        Q9npf7
                                                                                     <u>09kt16</u>
                                                                                                                                        Q95181
                                                                                                                                                   028747
                                                                                                                                                                                Q8mj75
                                                                                                                                                                                                                                                                                                                                           Description
                                                                                                                                                                                                                 28mke0
                                                                                                                                                                                                                                                         P35833
                                        3 bos taurus
7 sus scrofa
0 mus musculu
2 rattus norv
equus cabal
4 gallus gall
6 gallus gall
6 gallus scrofa
7 orcinus orc
7 orcinus cabal
2 homo sapien
5 homo sapien
6 vibrio chol
7 homo sapien
6 vibrio chol
8 sus scrofa
9 darosophila
geudomonas
stigmatella
homo sapien
```

<b>4</b> 5	44	43	42	41	40	39	38	37	36	<u>ω</u>	34	ω ω	32
84	84.5	84.5	84.5	85	85	85.5	85.5	86	86	86	86	96	86
9.3	9.4	9.4	9.4	9.4	9.4	9 5	9.5	9.5	9.5	9.5	9.5	9.5	9.5
175	455	211	209	208	193	1288	211	852	851	850	788	502	208
N	N	۲	Ь	N	N	N	N	N	N	N	N	N	ᅩ
Q9TTH4	Q7MDW7	IL6_LAMGL	IL6_PHOVI	Q6V919	Q9N2H9	QBLQRB	Q865W7	Q811T9	Q8CF88	Q7TQ21	Q8CF87	Q34008	IL6_BOVIN
		Q865x6 lama glama	Q28819 phoca vitul	Q6v919 bubalus bub		Q8lqr8 oryza sativ	Q865w7 camelus bac	Q811t9 mus musculu	Q8cf88 mus musculu	Q7tq21 mus musculu	Q8cf87 mus musculu	Q34008 beta vulgar	P26892 bos taurus

## ALIGNMENTS

D D D D D D D D D D D D D D D D D D D	R R R R R R R R R R R R R R R R R R R	RESULT OBNAW3 ID DT ODT ODD ODD ODD ODD ODD ODD ODD ODD
SEQUENCE FROM N.A.  TISSUB-Skin;  Straubberg R.;  Straubberg R.;  Straubberg R.;  Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.  EMBL; BC033245; AAH33245.1;  HSSP; P09919; IGNC.  GO; GO:0005576; C:extracellular; IEA.  GO; GO:0005125; F:cytokine activity; IEA.  GO; GO:0005128; F:interleukin-6 receptor binding; IEA.  GO; GO:0005138; F:interleukin-6 receptor binding; IEA.  InterPro; IFR003579; 4 helix cytokine.  InterPro; IFR003579; GCSF MGF.  InterPro; IFR003573; IL6 MGF GCSF.  InterPro; IFR003574; Interleukin_6.  Pfam; PF00489; IL6; 1.  PRINTS; PR00433; IL6GCSFMGF.	Preingold E.A., Grouse L.H., Derge J.G., Illins F.S., Wagner L., Shenmen C.M., Schuler eberg B., Buetow K.H., Schaefer C.F., Bhat N dan H., Moore T., Max S.I., Wang J., Hsieh F rusina K., Farmer A.A., Rubin G.M., Hong L., res M.B., Bonaldo M.F., Casavant T.L., Schee Usdin T.B., Toshiyuki S., Carninci P., Prang lano N.A., Peters G.J., Abramson R.D., Mulla n P.J., McKernan K.J., Malek J.A., Gunaratne ey K.C., Hale S., Garcia A.M., Gay L.J., Hul zny D.M., Sodergren B.J., Lu X., Gibbs R.A., E., Ketteman M., Wadan A., Rodrigues S., San A., Young A.C., Shevchenko Y., Bouffard G.G ouchman J.W., Green E.D., Dickson M.C., Chein M.A., Schmutz J., Myers R.M., Butterfi skalska U., Smailus D.E., Schnerch A., Schei M.A., M.A., Smailus D.E., Schnerch A., Schei nitial analysis of more than 15,000 full-len guences.";	1  1  BN4W3  PRELIMINARY;  PN8W4W3;  I-OCT-2002 (TrEMBLrel. 22, Cre  I-OCT-2002 (TrEMBLrel. 22, Las  I-MAR-2004 (TrEMBLrel. 26, Las  I-MAR-2004 (Tremblarel. 26, Las  I-MAR-2004 (Human)  I-MAR-2004 (Hum

```
PAR REPORTED AND REPORTED AND REPORTED AND REPORTED AND REPORT AND REPORTED AND REP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 2
CSF3_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SARARA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 174; Conser
                                                              "SeattleSNPs. NHLL."
FHCRC, Seattle, WA (UR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nagata S., I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-MAR-1989
01-MAR-1989
25-OCT-2004
SEQUENCE OF 19-207
MEDLINE=86151684;
Souza L.M., Boone
                                                                                                                                                                                  SEQUENCE FROM N.A.,
                                                                                                                                                                                                                                                                                                                                                                                     colony-stimulating factor."; EMBO J. 5:575-581(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Molecular cloning and expression colony-stimulating factor."; Nature 319:415-418(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE PROM N.A.
MEDLINE=86118679; PubMed=3484805;
Nagata S., Tsuchiya M., Asano S.,
Hirata Y., Kubota N., Oheda M., N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CSF3_HUMAN
P09919;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRINTS; PRO0434; INTERLEUKIN6.
ProDom; PD004358; GCSF MGF; 1.
ProDom; PD004356; Interleukin 6;
SMART; SM00126; IL6; 1.
                                                                                                                                                             Rieder M.J.,
                                                                                                                                                                                                                                                                                                     MEDLINE=87196936; Po
Devlin J.J., Devlin
                                                                                                                                                                                                                                                                                                                                                                                                                                               Oheda M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nagata
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Granulocyte
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PS00254; INTERLEUKIN_6; 1.
SEQUENCE 200 AA; 21543 MW; 8648AA55B329A96C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                      Nagata S., Tsuchiya M., Asano S., Ya
Dheda M., Nomura H., Yamazaki T.;
"The chromosomal gene structure and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=86220137; PubMed=2423327;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                            lines."
                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        domo sapiens (Human)
                                                                                                                                                                                                                                                               Expression of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (Filgrastim)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEELGMAPALQPTQGAMPAFASAFQRRAGGVLVASHLQSFLEVSYRVLRHLAQP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MBELGMAPALQPTQGAMPAFASAFQRRAGGVLVASHLQSFLEVSYRVLRHLAQP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LSSCPSQALQLAGCLSQLHSGLFLYQGLLQALEGISPELGPTLDTLQLDVADFATTIWQQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LSSCPSQALQLAGCLSQLHSGLFLYQGLLQALEGISPELGPTLDTLQLDVADFATTIWQQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TPLGPASSLPQSFLLKCLEQVRKIQGDGAALQEKLCATYKLCHPEELVLLGHSLGIPWAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TPLGPASSLPQSFLLKCLEQVRKIQGDGAALQEKLCATYKLCHPEELVLLGHSLGIPWAP
                                            19-207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (Rel. 10, Last sequence update)
(Rel. 45, Last annotation update)
colony-stimulating factor precursor (G-CSF)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                             Carrington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (Lenograstim)
                                                                                                                                                                                                                                                             granulocyte colony-stimulating
                                                                                                                                                                                                                       41:302-306(1987).
  PubMed=2420009;
T.C., Gabrilove
                                                                                                                                                                                                                                                                                                   PubMed=3494801;
in P.E., Myambo
                                         FROM N.A.
                                                                                 CORL:
                                                                                                                                                           AND VARIANTS MET-157 gton D.P., Chung M.-W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chordata;
Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99.4%;
                                                                                   the
      Gabrilove
                                                                               682 program for genom
http://pga.gs.washin
the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 896;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nomura l
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           , Kaziro i.,
Nomura H., Ono M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                     <u>۲</u>
    J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Yamamoto O.,
                                                                                                    for genomic apgeness.
                                                                                                                                                             M.-W.,
                                                                                                                                                                                                                                                                                                                                                                                                                             two mRNAs
                                                                                                                                                                                                                                                                                                   Lilly M.B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   207
  Lai
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6.9e-7
                                                                                                                                                                                AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BG
    P.H.,
                                                                                                                                                             ND THR-174.
Lee K.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Yamazaki T.,
                                                                                   databases
                                                                                                                                                                                                                                                               factor
                                                                                                                                                                                                                                                                                                                                                                                                                               for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hirata Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .3
                                                                                                    applications, on.edu).";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length
      Zsebo K.M.
                                                                                                                                                                                                                                                                                                       Rado T.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                             human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        granulocyte
                                                                                                                                                               Poel
                                                                                                                                                                                                                                                               γģ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (Pluripoietin)
                                                                                                                                                                                                                                                               human
                                                                                                                                                                                                                                                                                                                                                                                                                             granulocyte
                                                                                                                                                               C.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Kubota
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Yamamoto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0
                                                                                                                                                                                                                                                               cell
                                                                                                                         Ģ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        200
                                                                                                                                                               Υį
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61
```

EMBL;

X03438; M13008; X03656; X03655;

CAA27168.1; AAA03056.1; CAA27291.1; CAA277290.1;

entities roor send an

requires a license agreement ( an email to license@isb-sib.ch)

(See

http://www.isb-sib.ch/announce/

EMBL

outstation

g

```
This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Ew the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content modified and this statement is not removed. Usage by and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Clogston C.L., Hu S., Boone T.C., Lu H.S.; "Glycosidase digestion, electrophoresis and chromato of recombinant human granulocyte colony-stimulating produced in Chinese hamster ovary cells."; J. Chromatogr. A 637:55-62(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=93281718; PubMed=7685117;
Hill C.P., Osslund T.D., Elsenberg D.;
"The structure of granulocyte-colony-stimulating
relationship to other growth factors.";
Proc. Natl. Acad. Sci. U.S.A. 90:5167-5171(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=94304859; PubMed=7518249; Zink T., Ross A., Luers K., Cieslar C., "Structure and dynamics of the human grafactor determined by NMR spectroscopy. I bundle protein.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=93106200; PubMed=1281794; DOI=10.1016/0014-5793(92)81521-M; Zink T., Ross A., Ambrosius D., Rudolph R., Holak T.A.; "Secondary structure of human granulocyte colony-stimulating factor derived from NMR spectroscopy.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Barendt J., Platzer E., Moore M.A.S., Mertelsmann "Recombinant human granulocyte colony-stimulating normal and leukemic myeloid cells.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CARBOHYDRATE-LINKAGE SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Science
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Murdock D.C., Chazir
Barendt J., Platzer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    K-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Biochemistry 33:8453-8463(1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRUCTURE BY NMR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRUCTURE BY NMR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=93293942;
                                                                                                                                                                                                                                                         PTM: O-glycan consists of Gal-GalNAc disaccharide which can be modified with up to two sialic acid residues (done in recombinantly expressed G-CSF from CHO cells).

PHARMACEUTICAL: Available under the names Neupogen or Granulokine (Amgen/Roche) and Granocyte (Rhone-Poulenc). Used to treat neutropenia (a disorder characterized by an extremely low number of neutrophils in blood).

SIMILARITY: Belongs to the IL-6 superfamily.

CAUTION: Ref. 4 misquotes the gene name as "CSF1".

DATABASE: NAME=Neupogen/Granulokine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FUNCTION: Granulocyte/macrophage colony-stimulating factors at cytokines that act in hematopoiesis by controlling the product differentiation, and function of 2 related white cell population the blood, the granulocytes and the monocytes-macrophages.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUBCELLULAR LOCATION: Secreted ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUBUNIT: Monomer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      of the blood, the granulo CSF induces granulocytes.
                                                                                                                                                                                                                            WWW="http://www.neupogen.com/"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Name=Short;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Event=Alternative
                                                                                                                                                                                                                                             NOTE=Clinical information on Neupogen/Granulokine
                                                                                                                                                                                                                                                                                                                                                                                                                                             IsoId=P09919-2; Sequence=VSP_002673;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IsoId=P09919-1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    232:61-66(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                314:435-439(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chazin V.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PubMed=7685769;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence=Displayed,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bruszewski J., Lu H., (
ore M.A.S., Mertelsmann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C., Rudolph R., Holak T.A.;
granulocyte colony-stimulating
y. Loop mobility in a four-helix-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Lu H., Chen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              chromatographic mulating factor s
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         n R., Welt
g factor:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Holak T.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Welte
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           effects
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         populations
ophages. This
                                                                                                                                                                              a collaboration -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              production,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ဝ္ပ
```

```
RRR OCCOGNOTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ś
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DAC OCCUPANTA DE RESERVA DE COMPANIA DE RESERVA DE COMPANIA DE RESERVA DE RES
                                                                                                                                                                                                                                                                                                                                                                      RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Sin
Matches 141;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                            CANFA
                                                                                                                                                                                                     01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence up
25-OCT-2004 (Rel. 45, Last annotation
Granulocyte colony-stimulating factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Signal.
SIGNAL
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q9GJU0;
01-MAR-2001
01-MAR-2001
                                                                                    Canis familiaris (Dog).
Eukaryota; Metazoa; Chordata; (
Mammalia; Eutheria; Carnivora;
MCBI_TaxID=9615;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tsujimoto H., Hasegawa A., Ueda S.;
"Molecular cloning and expression of the
granulocyte colony-stimulating factor.";
Gene 274:263-269(2001).
                                                                                                                                                                                                                                                                                                   CSF3 CANFA
P35834;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR009079; 4 helix cytokine.
InterPro; IPR003629; GCSF MGF.
InterPro; IPR003573; IL6 MGF.GCSF.
InterPro; IPR003574; Interleukin_6.
Pfam; PF00489; IL6; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GO; GO:0005576; C:extraceliular; IEA.
GO; GO:0005125; F:cytokine activity; IEA.
GO; GO:0005138; F:interleukin-6 receptor binding; IEA.
GO; GO:000555; P:immune response; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AB042552; BAB17789.1; -. EMBL; AB042553; BAB17757.1; -. HSSP; P35834; 1BGE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Felis silvėstris catus (Cat).
Eukaryota; Metazoa; Chordata; (
Mammalia; Eutheria; Carnivora;
                     X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS)
MEDLINE=94076341; PubMed=7504736;
                                                                                                                                                                                      Name=CSF3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SMART; SM00126;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRINTS; PRO0433; IL6GCSFMGF.
PRINTS; PRO0434; INTERLEUKIN6.
PRODOM; PD008388; GCSF_MGF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Granulocyte
  Lovejoy B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE; PS00254; INTERLEUKIN_6; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=21531548; PubMed=11675019; Yamamoto A., Iwata A., Tuchiya K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=9685
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Name=G-CSF;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         05-JUL-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                          142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LSSCPSQALQLAGCLSQLHSGLFLYQGLLQALEGISPELGFTLDTLQLDVADFATTIWQQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TPLGPASSLPÓSFLLKCLEQVRKIQGDGAALQEKLCATYKLCHPEELVLLGHSLGIPWAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEELGMAPALQFTQGAMPAFASAFQRRAGGVLVASHLQSFLEVSYRVLRHLAQP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LSSCSSQALQLTGCLRQLHSGLFLYQGLLQALAGISPELAPTLDMLQLDITDFAINIWQQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TPLGPTSSLPQSFLLKCLEQVRKVQADGTALQERLCAAHKLCHPEELVLLGHALGIPQAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                195 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (TremBLrel. 16, Created)
(TremBLrel. 16, Last sequence update)
(TremBLrel. 27, Last annotation update)
colony-stimulating factor precursor.
    Cascio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         116;
.
D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                22 E
21255 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             82.6%;
81.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score
Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Potential.
; 544C682909412FCF CRC64;
                                                                                                              Craniata; Ve:
; Fissipedia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Craniata; Vertebrata;
; Fissipedia; Felidae;
                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         of the cDNA encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  744;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DOI=10.1016/S0378-1119(01)00575-3; Katsumata A., Oishi K., Saito T.,
                                                                                                                                                                                                                                                       update)
                                                                                                                                                                                                                                                                                                                           175
                                                                                                                                                                                                          update)
(G-CSF)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               S
                                                                                                                 Vertebrata;
ia; Canidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .4e-60;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BB
                                                                                                                                                                                                                                                                                                                           A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 195;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                 Euteleostomi; Canis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Euteleostomi;
Felis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              feline
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0
```

```
CSF3
                                                                                                                                                                                  밁
                                                                                                                        片
                                                                                                                                     Ś
                                                                                                                                                      밁
                                                                                                                                                                  Ş
                                                                                                                                                                                                                                                RESULT
                                                                                                                                                                                                  S
                                                                                                                                                                                                                 Matches 141;
                                                                                                                                                                                                                         Query Match
Best Local
Ovis aries (Sheep).
Eukaryota; Metazoa; (
Mammalia; Eutheria; (
Caprinae; Ovis.
NCBI_TaxID=9940;
                                   30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation updat:
Granulocyte colony-stimulating factor (G-CS)
Name=CSF3;
                                                                                  CSF3 S
                                                                                                                                                                                                                                                                                                  CARBOHYD
STRAND
HELIX
HELIX
TURN
HELIX
TURN
HELIX
TURN
HELIX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TURN
HELIX
TURN
HELIX
TURN
                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                      DISULFID DISULFID
                                                                                                                                                                                                                                                                                                                                                                                            PRINTS; PR00433; IL6GCSPMGF:
ProDom; PD008388; GCSF_MGF;
SMART; SM00126; IL6; 1
PROSITE; PS00254; INTERLEUKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                      -!- SIMILARITY: Belongs to the PDB; 1BGD; X-ray; @=1-175. PDB; 1BGB; X-ray; A/B=1-175.
                                                                                                                                                                                                                                                        STRAND
                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR009079; 4 helix cytokine.
InterPro; IPR003629; GCSF MGF.
InterPro; IPR003573; IL6_MGF_GCSF.
Pfam; PF00489; IL6; 1....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Crystal structure
                                                                                                                                                                                                                                                                                                                                                                                      D-structure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SUBUNIT: Monomer.
SUBCELLULAR LOCATION: Secreted.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CSF induces granulocytes.
                                                                                   SHEEP
                                                                                                                        121
                                                                                                                                      121
                                                                                                                                                      61
                                                                                                                                                                   61
                                                                                                                                                                                    <u>بــ</u>
                                                                                                                                                                                                  ш
                                                                                                                                                                                                                          Similarity
                                                                                                                                                      PLSSCPSQALQLAGCLSQLHSGLFLYQGLLQALEGISPELGFTLDTLQLDVADFATTIWQ
                                                                                                                       MAPLGPTGPLPQSFLLKCLEQMRKVQADGTALQETLCATHQLCHPEELVLLGHALGIPQP
                                                                                                                                                                                                  WILDEASSTEOSETTKCTEOAKIOGDGVATOSKTCVILKTCHEERTATTGHSTGIEMY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0-glycosylated
                                                                                                                                                                                                                                                175 AA;
                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                     10
12
45
63
67
72
93
101
144
                                                                                                                                                                                                                                                                                                                                                               3; Cytokine; Glycoprotein;
37 43
65 75
134 134 O-linked
                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                             INTERLEUKIN 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          of canine and bovine granulocyte-colony stimulating
                                                                                                                                                                                                                                                               Chordata; Craniat Cetartiodactyla;
                                                                                                                                                                                                                                                18858 MW;
                                                                                                                                                                                                                        82.0%;
                                                                                                                                                                                                                 Score 739; DB
Pred. No. 1.4e
11; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                            ۳.
                        Craniata; Vertebrata; Euteleostomi;
                                                                                   PRT;
                                                                                                                                                                                                                                                28C26B24990C6DB3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1L-6
                                                                                                                                                                                                                                                                                                                                                                                            щ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       superfamily.
                 Ruminantia;
                                                                                   174
                                             (G-CSF)
                                                                                                                                                                                                                                                                                                                                                                (GalNAc.
                                                                                                                                                                                                                                                                                                                                                                                      Growth
                                                                                   B
                                                                                                                                                                                                                                 BB
                                                                                                                                                                                                                         .4e-59;
                                                                                                                                                                                                                                  ,_
                                                                                                                                                                                                                  23;
                                                                                                                                                                                                                                                                                                                                                                                      factor.
                                                                                                                                                                                                                                                CRC64;
                                                                                                                                                                                                                                 Length 175;
                 Pecora;
                                                                                                                                                                                                                                                                                                                                                                ÷
                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                (By similarity).
                                                                                                                                                                                                                   0
                                                                                                                                                                                                                   Gaps
                                                                                                                          175
                                                                                                                                                       120
                                                                                                                                                                      120
                                                                                                                                                                                     60
                                                                                                                                                                                                   60
                                                                                                                                                                                                                   0
```

```
RESULT
CSF3_BC
 S
                                                                                                                                                                                                                                                                                                 밁
                                                                                                                                                                                                                                                                                                                             Ś
                                                                                                                                                                                                                                                                                                                                                             용
                                                                                                                                                                                                                                                                                                                                                                                       8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                              CSF3 BOVIN STANDARD; PRT; 195 AA. P35833; Q9TV89; 01-UN-1994 (Rel. 29, Created) 16-OCT-2001 (Rel. 40, Last sequence update) 25-OCT-2004 (Rel. 45, Last annotation update) Granulocyte colony-stimulating factor precursor Name=CSF3; Synonyms=GCSF; Bos taurus (Bovine).
Eukaryota; Metazoa; Chordata; Craniat
Mammalla; Eutheria; Cetartiodactyla;
Bovinae; Bos
NCBI_TaxID=9913;
                                                                                                                                                                              BOVIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PS00254; INTERLEUKIN 6; 1.
Cytokine; Glycoprotein; Growth fact
DISULFID 36 42 By Sir
DISULFID 64 74 By Sir
CARBOHYD 133 133 O-link
SEQUENCE 174 AA; 18806 MW; BASA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    the European Bioinformatics Institute. There use by non-profit institutions as long as modified and this statement is not removed. U
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIJINE=95102116; PubMed=7528579;
O'Brien P.M., Seow H.F., Rothel J.S.
"Cloning and sequencing of an ovine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SMART; SM00126;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HSSP; P09919; 1RHG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; L07939; AAA68006.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Cloning and sequencing of an factor cDNA.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRINTS; PR00433; IL6GCSFMGF.
ProDom; PD008388; GCSF_MGF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00489; IL6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR009079; 4 helix cytokine. InterPro; IPR003629; GCSF MGF. InterPro; IPR003573; IL6 MGF GCSF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         [1]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                    Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PTM: O-glycosylated (By similarity). SIMILARITY: Belongs to the IL-6 superfamily.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Seq. 4:339-342(1994).
FUNCTION: Granulocyte/macrophage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUBCELLULAR LOCATION: Secreted.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cytokines that act in hematopolesis by controlling the product differentiation, and function of 2 related white cell population the blood, the granulocytes and the monocytes-macrophages.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUBUNIT: Monomer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              T10268; T10268.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation - Buropean Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                     143;
                                                                                                                                                                                                                                                                    122
                                                                                                                                                                                                                                         121
                                                                                                                                                                                                                                                                                                 61
                                                                                                                                                                                                                                                                                                                               62
                                                                                                                                                                                                                                                                                                                                                             ۳
                                                                                                                                                                                                                                                                                                                                                                                         N
                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      induces granulocytes (By similarity).
                                                                                                                                                                                                                                                          MEELGMAPALQPTQGAMPAFASAFQRRAGGVLVASHLQSFLEVSYRVLRHLAQP
                                                                                                                                                                                                                                     MEDLGVAPAVOPTQGTMPTFTSAFQRRAGGVLVASQLQRFLGLAYRGLRYLAEP
                                                                                                                                                                                                                                                                                                 LSSCSSQSLQLTSCLDQLHGGLFLYQGLLQALAGISPELAPTLDTLQLDVTDFATNIWLQ
                                                                                                                                                                                                                                                                                                                   LSSCPSQALQLAGCLSQLHSGLFLYQGLLQALEGISPELGPTLDTLQLDVADFATTIWQQ
                                                                                                                                                                                                                                                                                                                                                             TPLGPARSLPQSFLLKCLEQVRKIQADGAELQERLCATHKLCHPEELVLLGHSLGIPQAP
                                                                                                                                                                                                                                                                                                                                                                            TPLGPASSLPQSFLLKCLEQVRKIQGDGAALQEKLCATYKLCHPEELVLLGHSLGIPWAP
                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IL6;
                                                                                                                                                                                                                                                                                                                                                                                                                                   81.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .
                                                                                                                                                                                                                                                                                                                                                                                                                      10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              By similarity.
By similarity.
O-linked (GalNAc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score
                                                                                                                                                                                                                                                                                                                                                                                                                                    Pred.
                                          Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BASAA8F8D23ACD1E CRC64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           J.S.,
                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                    738;
No. 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             granulocyte
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  colony-stimulating tis by controlling t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Wood P.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (See http://www.isb-sib.ch/announce,
                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 1;
.7e-59;
                                                                                                                                                                                                                                                                                                                                                                                                                      21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            colony-stimulating
                                                                                     (G-CSF)
                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (By similarity)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                factors are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ne production,
l populations
rophages. This
                                                                                                                                                                                                                                                                                                                                                                                                                     0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       for
                                                                                                                                                                                                                                                                    175
                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                               121
                                                                                                                                                                                                                                                                                                                                                           60
                                                                                                                                                                                                                                                                                                                                                                                         61
                                                                                                                                                                                                                                                                                                 120
```

중 음 중

62 2

LSSCPSQALQLAGCLSQLHSGLFLYQGLLQALEGISPELGPTLDTLQLDVADFATTIWQQ 121

TPLGPARSLPQSFLLKCLEQVRKIQGDOAALQRKLCATYKLCHPEELVLLGHSLGIPQAP

18

```
Query Match
Best Local S
Matches 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           factor (G-CSF). J. Mol. Biol. 23
                                       HELIX
TURN
SEQUENCE
                                                                                                                                                                                    DISULFID
DISULFID
CARBOHYD
CONFLICT
                                                                                  T SE
                                                                                          HELIX
TURN
HELIX
TURN
HELIX
TURN
                                                                                                                                                      HELIX
HELIX
TURN
                                                                                                                                                                                                                                                                                                     Pfam;
                                                                                                                                                                                                                                                                                                                                                                          use by non-profit institutions as long modified and this statement is not removed. entities requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced between the Swiss Institute of Bioinformatics and the European Bioinformatics Institute. There are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      - -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              colony stimulating fasting submitted (SEP-1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=Holstein;
Heidari M., Kehrli M.E.
"Cloning, sequencing, a:
                                                                                                                                                                                                                              CHAIN
                                                                                                                                                                                                                                        SIGNAL
                                                                                                                                                                                                                                                                       SMART;
                                                                                                                                                                                                                                                                             PRINTS; PRO0433; IL6GCSFMGF.
ProDom; PD008388; GCSF_MGF; 1.
                                                                                                                                                                                                                                                                                                             InterPro; IPR009079; 4 helix cytokine
InterPro; IPR003629; GCSF MGF.
InterPro; IPR003573; IL6_MGF_GCSF.
                                                                                                                                                                                                                                                                                                                                                      EMBL; AF092533; AAD16102.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Lovejoy B., Cascio D., Eisenberg D.; "Crystal structure of canine and bovine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              [1]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                            PROSITE; PS00254;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         -!- SIMILARITY: Belongs to the IL-6 superfamily.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=94076341; PubMed=7504736;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         X-RAY CRYSTALLOGRAPHY (1.7 ANGSTROMS).
                                                                                                                                                                                                                                                  D-structure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUBCELLULAR LOCATION: Secreted. PTM: O-glycosylated.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUBUNIT: Monomer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 differentiation, and function of the blood, the granulocytes CSF induces granulocytes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FUNCTION: Granulocyte/macrophage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cytokines that act
                                                                                                                                                                                                                                                                                                                                              1BGC;
 141;
                                                                                                                                                                                                                                                                                                    PF00489; IL6; 1
                                                                                                                                                                                                                                                                      SM00126; IL6; 1.
         Similarity
                                                                                                                                                                                                                                                                                                                                 IPR009079;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sequencing, and analysis of cDNA encoding bovine imulating factor.";
                                         195
 Conservative
                                                                                          154
93
32
65
70
72
72
78
83
87
92
                                                                                                                                                                                                                                         Cytokine;
                                        A
A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       234:640-653 (1993)
                                                                                                                                                                                                                                                           INTERLEUKIN_6; 1
                                                                     192
21431 MW;
       80.7%;
81.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       et in hematopoiesis and function of 2 r
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Jr.;
11;
Score 727; DB
Pred. No. 1.9e
11; Mismatches
                                                                                                                                                                                     O-linked
TS -> RG
                                                                                                                                                                                                                             Granulocyte colony-stimulating factor.
                                                                                                                                                                                                                                        Potential
                                        8C06119E4ADFBA73 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             of 2 related white cell populat and the monocytes-macrophages.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 colony-stimulating tsis by controlling t
                                                                                                                                                                                     (GalNAc.
                                                                                                                                                                                                                                                  Growth factor; Signal
                                                                                                                                                                                                                                                                                                                                                                                     oved. Usage by and to (See http://www.isb-sib
                                                                                                                                                                                                                                                                                                                                                                                                      There are no restrictions ng as its content is in
         DB 1;
.9e-58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          granulocyte-colony
                                                                                                                                                                                     2).
                  Length
                                                                                                                                                                                                                                                                                                                                                                                                                            and the
                                                                                                                                                                                              ٠.
 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                      through
                                                                                                                                                                                               (By similarity)
                                                                                                                                                                                                                                                                                                                                                                                               λq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  the
                                                                                                                                                                                                                                                                                                                                                                                                and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             factors
                                                                                                                                                                                                                                                                                                                                                                                                                                IBMB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           stimulating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 granulocyte
                                                                                                                                                                                                                                                                                                                                                                                                                                       a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  production,
0
                                                                                                                                                                                                                                                                                                                                                                                                for
                                                                                                                                                                                                                                                                                                                                                                                       .ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                outstation
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             are
                                                                                                                                                                                                                                                                                                                                                                                                                    9
                                                                                                                                                                                                                                                                                                                                                                                                           ö
 0
```

```
RESULT 8
                                     밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ś
Query Match
Best Local Similarity
                                    DISULFID
DISULFID
CARBOHYD
CONFLICT
SEQUENCE
                                                                                                                                               PRINTS; PR00433; IL6GCSFMGF.
ProDom; PD008388; GCSF_MGF; 1.
SMART; SM00126; IL6; 1.
                                                                                                                                                                                                                                                                                                                                                                             This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gloster S.E., Sandeman R.M., "Cloning of a cDNA and gene stimulating factor.";
Submitted (SEP-1997) to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bukaryota; Metazoa;
Mammalia; Butheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30-MAY-2000 (Rel. 39, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Granulocyte colony-stimulating factor precursor
Name=CSF3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CSF3
                                                                                                                                                                                                                                                  EMBL; U68482;
EMBL; U68481;
                                                                                                                                                                                                                                                                            EMBL; Y10494;
                                                                                                                                                                                                                                                                                                     or send an
                                                                                                                                                                                                                                                                                                                             modified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sus scrofa (Pig).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          002837; 019:
15-JUL-1998
                                                                                                  CHAIN
                                                                                                             SIGNAL
                                                                                                                          Cytokine;
                                                                                                                                     PROSITE; PS00254;
                                                                                                                                                                                       InterPro; IPR003573
Pfam; PF00489; IL6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE=Liver;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (JAN-1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kulmburg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=9823;
                                                                                                                                                                                                                nterPro;
                                                                                                                                                                                                                           nterPro;
                                                                                                                                                                                                                                                                                                  European Bioinformatics Institute. There are no rest
by non-profit institutions as long as its content
ified and this statement is not removed. Usage by an
ities requires a license agreement (See http://www.isb-
send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                    FUNCTION: Granulocyte/macrophage colony-stimulating factors are cytokines that act in hematopolesis by controlling the production, differentiation, and function of 2 related white cell populations of the blood, the granulocytes and the monocytes-macrophages. This CSF induces granulocytes (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                   PTM: O-glycosylated (By similarity). SIMILARITY: Belongs to the IL-6 superfamily.
                                                                                                                                                                                                                                                                                                                                                                                                                              SUBCELLULAR LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                           SUBUNIT: Monomer.
                                                                                                                                                                                                                                                                                                                                                              SWISS-PROT entry is copyright. It is produced through en the Swiss Institute of Bioinformatics and the EN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         019180;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .
סי
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEELGMAPALQPTQGAMPAFASAFQRRAGGVLVASHLQSFLEVSYRVLRHLAQP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIGAAPAVOPTOGAMPTFTSAFORRAGGVLVASQLHRFLELAYRGLRYLAEP 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IPR009079; 4 helix cytokine IPR003629; GCSF MGF. IPR003573; IL6 MGF GCSF.
                                                                                                                          Glycoprotein;
                                     195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (Rel.
                                                 1
22
57
85
154
123
                                                                                                                                                                                                                                                               CAA71518.1; -.
AAB70701.1; -.
                                                                                                                                                                                                                                        1RHG
                                                                                                                                                                                                                                                  AAB70700.1; -.
                                     8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           36, Created)
                                                                                                                        INTERLEUKIN 6; 1.
otein; Growth factor; Signal.
                                                                          195
63
95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chordata; Craniata; Vertebrata;
Cetartiodactyla; Suina; Suidae;
                                    21214
77.9%;
79.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Я.М.,
                                     3
.
                                                                                                                                                                                                                                                                                                                                                                                                                              Secreted
                                       Potential.

Granulocyte colony-stimulating fa Granulocyte colony-stimulating fa By similarity.

By similarity.

O-linked (GalNac. . .) (By simil A -> R (in Ref. 1).

A -> R (in Ref. 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       strom A.D.G.;
encoding porcine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL/GenBank/DDBJ databases
Score 702; DB 1;
Pred. No. 3.8e-56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                     84787F20DB0AEA1C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A
                                                                                                                                                                                                                                                                                                                http://www.isb-sib
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            granulocyte-colony
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   databases
           Length 195;
                                     CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (G-CSF)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Euteleostomi;
Sus.
                                                                                                                                                                                                                                                                                                                                                      restrictions
                                                                                                                                                                                                                                                                                                                             and
                                                              similarity)
                                                                                                                                                                                                                                                                                                                                                                  EMBL
                                                                                                                                                                                                                                                                                                                                                                  a collaboration
                                                                                                   factor
                                                                                                                                                                                                                                                                                                                  .ch/announce/
                                                                                                                                                                                                                                                                                                                                           덩
                                                                                                                                                                                                                                                                                                                                                      음
```

```
RESULT 9
CSF3 M
AC P09920
DT CSF3 M
AC P09920
DT 01-MAR
DT 01-MAR
DT 01-MAR
DT 01-MAR
DT 05-JULI
GN Name=C
OS Mus mu
OC Mammal
OX NCBI_T
RN [1]
RP SEQUEN
RA TSUChi
RT "Isola
RT POCC
RN [2]
RP SEQUEN
RA TSUChi
RT POCC
RN [2]
RP SEQUEN
RA TSUChi
RT FACCO
RN [2]
RP PARTIA
RY PUBMEd
RA Simpso
RT factor
RI Biol.
CC -!- SU
CC -!- SU
CC -!- SI
CC -!- 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             맑
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ś
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        05-JUL-2004 (Rel. 44, Last annotation update)
Granulocyte colony-stimulating factor precursor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=87190474; PubMed=3494605;
MEDLINE=87190474; PubMed=3494605;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Name=Csf3; Synonyms=Csfg;
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-MAR-1989 (Rel. 10, Last sequence up 05-JUL-2004 (Rel. 44, Last annotation
                                                                                              EMBL; M13926;
EMBL; X05402;
                                                                                                                                                                  or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                modified
                                                                                                                                                                                                                                                                                       between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PubMed=3501294;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eur. J. Biochem.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "The chromosomal gene structure stimulating factor.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   colony-stimulating factor."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=87017003; PubMed=3489940;
Tsuchiya M., Asano S., Kaziro Y., Nagata S.;
"Isolation and characterization of the cDNA for murine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-MAR-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           P09920;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Simpson R.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PARTIAL SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mammalia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          actor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Structural studies
                                                                                                                                                                                                         European Bioinformatics Institute. The by non-profit institutions as long ified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                      SUBCELLULAR LOCATION: Secreted. PTM: O-glycosylated (By similarity). SIMILARITY: Belongs to the IL-6 superfamily.
                                                                                                                                                                                                                                                                                                                                                                                                                            SUBUNIT: Monomer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FUNCTION: Granulocyte/macrophage colony-stimulating cytokines that act in hematopoiesis by controlling t differentiation, and function of 2 related white cel
                                                                                                                                                                                                                                                                                  SWISS-PROT entry is copyright. It is produced through sen the Swiss Institute of Bioinformatics and the EM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Natl. Acad.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   137;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chem. Hoppe-Seyler 368:1327-1331(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          the blood,
                                                                                                                                                                                                                                                                                                                                                                                                                                                  induces granulocytes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SSCPSQALQLAGCLSQLHSGLFLYQGLLQALEGISPELGPTLDTLQLDVADFATIIWQQM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PLSPASSLPQSFILKCLEQVRKIQADGAELQERLCATHKLCHPQELVLLGHSLGLPQASL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PLGPASSLPQSFLLKCLEQVRKIQGDGAALQEKLCATYKLCHPEELVLLGHSLGIPWAPL
                                                                                                                                                                                          requires a license agreement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EDLRMAPASLPTOGTVPTFTSAFORRAGGVLVVSQLQSFLELAYRVLRYLAEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EELGMAPALQPTQGAMPAFASAFQRRAGGVLVASHLQSFLEVSYRVLRHLAQP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SSCSSQALQLTGCLNQLHGGLVLYQGLLQALAGISPELAPALDILQLDVTDLATNIWLQM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                              AAA37672.1;
CAA28986.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nice
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    165:7-12(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sci.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        on, and function of 2 related white cell population, and function of 2 related white cell population.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        t×1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                on the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     <u>;</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  U.S.A. 83:7633-7637(1986)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nicola N...
he murine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Α.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                granulocyte colony-stimulating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  murine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      208
                                                                                                                                                                                             (See
                                                                                                                                                                                                                                      There are no rest
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A
                                                                                                                                                                                          http://www.isb-sib.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                granulocyte colony-
                                                                                                                                                                                                              Usage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (G-CSF)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                   ý
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Murinae; Mus.
                                                                                                                                                                                                                                                              restrictions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                granulocyte
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 factors
                                                                                                                                                                                                                                                                                         EMBL outstation
                                                                                                                                                                                                                                                                                                                 ω
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        production,
                                                                                                                                                                                                                     for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0
                                                                                                                                                                                                                                                                                                            collaboration
                                                                                                                                                                                          .ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                             20 G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0
```

PIR; A29536; A26496. HSSP; P09919; 1RHG.

InterPro;

MGI:1339751; Csf3. rPro; IPR009079; 4\_helix\_cytokine.

1RHG.

```
RESULT 10
P97712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ś
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ś
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5
Query Match 70.9
Best Local Similarity 72.0
Matches 127; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches 129;
                                                                                                                                                 60; ഒ ഒ ഒ ഉ
                                                                                                                                                                                                                                                                                                                                                                                       P97712;
01-MAY-1997
:01-MAY-1997
                                           PRINTS; PRO0433; ILGGCSFMGF.
PRODOM; PD008388; GCSF MGF; 1.
SMART; SM00126; ILG; 1.
PROSITE; PS00254; INTERLEUKIN 6;
SEQUENCE 214 AA; 23659 MW; 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Signal.
SIGNAL
                                                                                                                                                PIR; JC5043; JC5043.

HSSP; P09919; IRHG.
GO; GO:0005576; C:extracellular; IEA.
GO; GO:0005125; F:cytokine activity; IEA.
GO; GO:0008083; F:growth factor activity;
GO; GO:0006955; P:immune response; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DISULFID
DISULFID
CARBOHYD
                                                                                                      InterPro; IPR009079; 4 helix_cytokine.
InterPro; IPR003629; GCSF MGF.
InterPro; IPR003573; IL6_MGF_GCSF.
Pfam; PP00489; IL6; 1.
                                                                                                                                                                                                                                                        MEDLINE=97074656; PubMed
Han S.W., Ramesh N., Osb
"Cloning and expression
                                                                                                                                                                                                                       Gene 175:101-104(1996).
EMBL; U37101; AAC52915.1; -.
                                                                                                                                                                                                                                               stimulating factor."
                                                                                                                                                                                                                                                                                                                             Granulocyte colony stimulating factor.
Rattus norvegicus (Rat)
Bukaryota, Metazoa; Chordata; Craniata
Mammalia; Eutheria; Rodentia; Sciurogn
                                                                                                                                                                                                                                                                                                                                                                            01-MAY-1997 (TrEMBLrel.
01-MAR-2004 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                          P97712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRINTS; PRO0433; ILGGCSFMGF.
ProDom; PD008388; GCSF_MGF; 1.
ProDom; PD004356; Interleukin_6; 1.
SMART; SM00126; IL6; 1.
                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cytokine; Direct protein sequencing; Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PS00254; INTERLEUKIN_6; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PF00489; IL6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ш
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MTPLGPASSLPQSFLLKCLEQVRKIQGDGAALQEKLCATYKLCHPEELVLLGHSLGIPWA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QMENLGVAPTVQPTQSAMPAFTSAFQRRAGGVLAISYLQGFLETARLALHHLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QMEELGMAPALQPTQGAMPAFASAFQRRAGGVLVASHLQSFLEVSYRVLRHLA 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SLSGCSSQALQQTQCLSQLHSGLCLYQGLLQALSGISPALAPTLDLLQLDVANFATTIWQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PLSSCPSQALQLAGCLSQLHSGLFLYQGLLQALEGISPELGFTLDTLQLDVADFATTIWQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VSALPPSLPLPRSFILKSLEQVRKIQASGSVLLEQUCATYKLCHPEELVLLGHSLGIPKA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IPR003573; IL6_MGF_GCSF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1
31
72
100
169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ă,
                                                                                                                                                                                                                                                                     PubMed=8917083; DOI=10.1016/0378-1119(96)00131-X;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30
208
78
110
169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       71.3%;
74.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22421 MW;
          70.5%;
                                                                                                                                                                                                                                                          Osborne W
                                                                                                                                                                                                                                                                                                                                                                          03, Created)
03, Last sequence update)
26, Last annotation update)
  12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11;
Score 635; DB
Pred. No. 5.6e
12; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Granulocyte colony-stimulating By similarity.
By similarity.
O-linked (GalNAc. . .) (By simil
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score
                                                                                                                                                                                                                                                                                                                             Craniata; Vert
Sciurognathi;
                                                                                                                                                                                                                                                        cDNA encoding
                                           ; 1.
29BB88B17B684C55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0BF3622135C906DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       642; DB 1;
No. 1.2e-50;
                                                                                                                                                                                                                                                                                                                             Vertebrata; |
thi; Muridae;
          DB 2;
.6e-50;
                                                                                                                                                                                                                                                                                                                                                                                                                          Ä
                                                                                                                                                                                                                                                          rat
                     Length
                                              CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CRC64
                                                                                                                                                                                                                                                         granulocyte colony
 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Growth factor;
                                                                                                                                                                                                                                                                                                                              Euteleostomi;
; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (By similarity)
 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     60
0
```

```
RESULT 12

MGF CHICK STAN

ID MGF CHICK STAN

AC P13854;

DT 01-JAN-1990 (Rel. 1

DT 01-JAN-1990 (Rel. 1

DT 28-FEB-2003 (Rel. 2

DE Myelomonocytic grow

OS Gallus gallus (Chic.
                                                                                                                                                           S
                                                                                                                                                                                      밁
                                                                                                                                                                                                         S
                                                                                                                                                                                                                                      밁
                                                                                                                                                                                                                                                            S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT
Q8MKE0
                                                                                                                                                                                                                                                                                                                                       S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              - 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5
                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                 Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ul-OCT-2002 (TrEMBLrel. 22, Creat
01-OCT-2002 (TrEMBLrel. 22, Last
01-MAR-2004 (TrEMBLrel. 26, Last
Granulocyte colony-stimulating fa
Name=G-CSF;
                                                                                                                                                                                                                                                                                                                                                            Pfam; PF00489; IL6; 1.
PRINTS; PR00433; IL6GCSFMGF.
PRODOm; PD008388; GCSF_MGF;
SMART; SM00126; IL6; 1.
                                                                                                                                                                                                                                                                                                                                     PROSITE; PS00254; INTERLEUKIN_6; 1. SEQUENCE 127 AA; 13657 MW; 2555
                                                                                                                                                                                                                                                                                                                                                                                                                                                GO; GO:0005576; C:extracellular; IEA.
GO; GO:0005125; F:cytokine activity; IEA.
GO; GO:0008083; F:growth factor activity;
GO; GO:0006955; P:immune response; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AF503365; AAM34205.1;
HSSP; P35833; 1BGC:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (APR-2002)
                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR009079; 4 helix cytok
InterPro; IPR003629; GCSF MGF.
InterPro; IPR003573; IL6 MGF GCSF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q8MKE0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Noronha L.E., Takafuji V.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=9796
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Equus caballus (Horse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q8MKE0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11
                                                                                                                                                                                                                                                                                    101;
                                                                                                                                     121
                                                                                                                                                              169
                                                                                                                                                                                                               109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  147
                                                                                                                                                                                      61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121
                                                                                                                                                                                                                                                              49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 27
                                                                                                                                                                                                                                      ш
                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LRYLAEP
                                                                                                                                                              LRHLAQP 175
                                                                                                                                                                                                             LDVADFATTIWQQMEELGMAPALQPTQGAMPAFASAFQRRAGGVLVASHLQSFLEVSYRV 168
                                                                                                                                                                                                                                                             VILIGHSLGIPWAPLSSCPSQALQLAGCLSQLHSGLFLYQGLLQALEGISPELGPTLDTLQ
                                                                                                                                                                                      LDVTDFATNIWQQMEDLGVAPVVQPTHGPMPTFASAFQRRAGGVLVASNLQRFLELAYRG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PLSSCPSQALQLAGCLSQLHSGLFLYQGLLQALEGISPELGPTLDTLQLDVADFATTIWQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QMESLGVAPTVQPTQSTMPIFTSAFQRRAGGVLVTSYLQSFLETAHHALHHLPRP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QMEELGMAPALQPTQGAMPAFASAFQRRAGGVLVASHLQSFLEVSYRVLRHLAQP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SLSSCSSQALQQTKCLSQLHSGLFLYQGLLQALAGISSELAPTLDMLHLDVDNFATTIWQ
                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                          STANDARD;
                                                                                                                                     127
                                                                                                                                                                                                                                                                                              56.7%;
79.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Chordata; Craniata; Vertebrata; Perissodactyla; Equidae; Equus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           to the
                                                                                                                                                                                                                                                                                                                                                                                                                            helix_cytokine.
                                                                                                                                                                                                                                      SQALQUIGCUSQUESGULLYQGULQALAGISPELAPTLDMLQ
                                                                                                                                                                                                                                                                                     9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          , Sharova L.V., Crisman EMBL/GenBank/DDBJ datab
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Created)
                                                                                                                                                                                                                                                                                    Score 511; DB 2
Pred. No. 7e-39;
Mismatches
                                                                                                                                                                                                                                                                                                                                      25559C2569802077
                                                                          201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     127
                                                                          ⋛
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                IEA.
                                                                                                                                                                                                                                                                                                            2
                                                                                                                                                                                                                                                                                    17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           databases
                                                                                                                                                                                                                                                                                                            Length 127;
                                                                                                                                                                                                                                                                                                                                      CRC64;
                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       M.V.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Howard
                                                                                                                                                                                                                                                                                     0,
                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R.D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  201
                                                                                                                                                                                       120
                                                                                                                                                                                                                                      60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         60
```

Rel. 13, Created)
Rel. 13, Last sequence update)
Rel. 41, Last annotation updat
Rel. 41, Cast annotation (MGF
c growth factor precursor (MGF
(Chicken).

n update) or (MGF).

200

```
Matches
                                                                                                                                                                                                                    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                          DISULFID
DISULFID
CARBOHYD
CARBOHYD
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRINTS; PR00433; ILGGCSFMGF.
PRINTS; PR00434; INTERLEUKIN6.
PRODOM; PD008388; GCSF MGF; 1.
PRODOM; PD004356; Interleukin_6; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EW the European Bioinformatics Institute. There are no restrue by non-profit institutions as long as its content
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sterneck E., Blattner C., Graf T., Leutz A.; "Structure of the chicken myelomonocytic grospecific activation of its promoter in avian
                                                                                                                                                                                                                                                                                                                                                                                                                        SMART; SM00126; IL6; PROSITE; PS00254; IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; M85034; AAA48694.1; EMBL; X14477; CAA32639.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   entities requires a license agreement (sor send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      use by non-profit institutions as long modified and this statement is not removed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Molecular cloning of the chicken myelomonocytic growth factor reveals relationship to interleukin 6 and granulocyte colony stimulating factor.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Archosauria; Aves; Gallus.
                                                                                                                                                                                                                                                                                                                                                                     CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR003574
Pfam; PF00489; IL6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
MEDLINE=92195319; PubMed=1549124;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Leutz A., Damm K., Sterneck E.,
Gausepohl H., Pan Y.-C.E., Smari
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=9031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PIR; A42247; A42247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          protein kinases."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBO J. 8:175-181(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=89231616; PubMed=2785450;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            [nterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         nterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SIMILARITY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FUNCTION: Hematopoietic growth fact proliferation and colony formation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SUBCELLULAR LOCATION: Secreted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cells of the myeloid lineage.
132 QPTQ--GAMPAFASAFQRRAGGVLVASHLQSFLEVSYRVLRHLAQ 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          P09919; 1RHG
                                                                                                                             36
                                                       96 AEVCFTQIRAGLHAYHDSLGAVLRLLPNHTTLVETLQLDAANLSSNIQQQMEDLGLDTVT
                                                                                           72
                                                                                                                                                                                                     67;
                                                                                           LAGCLSQLHSGLFLYQGLLQALEGISPELGFTLDTLQLDVADFATTIWQQMEELGMAPAL
                                                                                                                               QLFLHKNLEFTRKIRGDVAALQRAVCDTFQLCTEEELQLVQPDPHLVQAPLDQCHKRGFQ
                                                                                                                                                               OSELTKCTEOAKIOGDGYATOEKTCALAKTCHEBETATTGH8TG1EMYET88CE8OATO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IPR009079; 4 helix cytokine.
IPR003629; GCSF_MGF.
IPR003573; IL6_MGF_GCSF.
IPR003574; Interleukin_6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Biol. 12:1728-1735(1992).
                                                                                                                                                                                                                                                                                                              24
61
89
123
                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                             B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Belongs to the IL-6 superfamily.
                                                                                                                                                                                                                                                                                                                                                                                                     INTERLEUKIN 6; 1. wth factor; Signal.
                                                                                                                                                                                                                                                                            201
67
99
123
137
22373
                                                                                                                                                                                                                      33.7%;
                                                                                                                                                                                                                                                                             ₹
;
                                                                                                                                                                                                   28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Smart J., Hayman M.,
                                                                                                                                                                                                                                                                                             Myelomonocytic growth fa
By similarity.
By similarity.
N-linked (GlcNAc. . .) N-linked (GlcNAc. . . )
                                                                                                                                                                                                                      Score 304; DB 1
Pred. No. 1e-19;
                                                                                                                                                                                                                                                                            240A8DD21B4244E6 CRC64;
                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               avian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            growth factor gene vian myelomonocytic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       normal and trans
                                                                                                                                                                                                                                       1.
                                                                                                                                                                                                     68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Usage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         S., Graf
                                                                                                                                                                                                                                     Length 201;
                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                     factor.
                                                                                                                                                                                                                                                                                               (Potential). (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Frank R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         transformed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        restri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TEMBL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               and
cells
                                                                                                                                                                                                   <u>ب</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ctions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (cMGF
                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         avian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               λĢ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ဋ
                                                          155
                                                                                           131
                                                                                                                                                                   71
                                                                                                                               95
                                                                                                                                                                                                   ٠,
```

ţ,

ą В Ś 밁 δ

```
S
                                                                               밁
                                                                                                                    5
                                                                                                                                                                                                   Ś
                                                                                                                                                                                                                                                 밁
                                                                                                                                                                                                                                                                                                                                                                                                                     SOUTH TEACH TO THE TEACH TO THE
문
                                                                                                                                                                문
                                                                                                                                                                                                                                                                                      8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         뭐
                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local S
                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                     CHAIN
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Signal.
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GO; GO:0005138; F:interleukin-6 receptor binding; GO; GO:0005138; F:interleukin-6 receptor binding; GO; GO:0005138; F:imterleukin-6 receptor binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRINTS; PR00433; IL6GCSFMGF.
PRINTS; PR00434; INTERLEUKIN6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases EMBL; AJ309540; CAC40812.1; -. EMBL; AJ250838; CAC15566.2; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Salmonella gallinarum.";
Microbiology 146:3217-3226(2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. Schneider K., Klaas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gallus gallus (Chicken).
Gallus gallus (Chicken).
Gallus gallus (Chicken).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              05-JUL-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; 01Y060
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OIXO6D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ProDom; PD008388; GCSF_MGF; 1.
ProDom; PD004356; Interleukin_6; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Kaiser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Wigley P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Kaiser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (FEB-2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gallus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Name=11-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=9031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Archosauria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Interleukin-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Differential cytokine expression in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               invasion by Salmonella
                                       154
                                                                                 157
207 IEKITMHLILRDFTSFMEKTVRAVRYL
                                                                                                                      100
                                                                                                                                                                  101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      156 LPAEQRSPPPTFSGPFQQQVGGFFILANFQRFLETAYRALRHLAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             P052
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PF00489;
                                                                                                                                                                                                         4
                                                                                                                                                                                                                                                   41
                                                                                                                                                                                                                                                                                                                                      46;
                                                                                                                                                                                                                                                                                             4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              שי
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SMOOL
                                                                                                                                                                                                                                                                                                                                                        Similarity
                                       ---VASHL-----QSFLEVSYRVLRHL
                                                                                                                      LGPTLDTLQLDVADFATTIWQQMEELGMAPALQPTQGAMPAFASAFQRRAGGVL-
                                                                                                                                                                  NSMEMLVRNNLNLP----KVTEEDGCLLAGFDEEKCLTKLSSGLFAFQTYLEFIQETFDS
                                                                                                                                                                                                         PEETVILGHSIGIPWAPLSSCPSQALQLAG----CLSQLHSGLFLYQGLLQALEGISPB
                                                                                                                                                                                                                                                 LPPAAAVPLPAAADSSGEVGLEEEAGARRALLDCEPLARVLRDRAVQLQDEMCKKFTVCE
                                                                                                                                                                                                                                                                                           LGPASSLP---------QSFLLKCLEQVRKIQGDGAALQEKLCATYKLCH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FROM N.A.
                                                                                 EKONVESICYSTKHLAATIROMV----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rothwell
                                                                                                                                                                                                                                                                                                                                                                                                                     241
                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Aves;
                                                                                                                                                                                                                                                                                                                                                                                                                                           48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          precursor
                                                                                                                                                                                                                                                                                                                                                                                                                     ă,
                                                                                                                                                                                                                                                                                                                                                                                                                     47 P
241 m
26790 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INTERLEUKIN_6; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ľ.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                æ
                                                                                                                                                                                                                                                                                                                                                            12.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ç
                                                                                                                                                                                                                                                                                                                                                 . 2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               typhimurium,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Galyov E.E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kaspers B., Staeheli i
the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              19,
19,
27,
                                                                                                                                                                                                                                                                                                                                      35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Last
Last
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Created)
                                                                                                                                                                                                                                                                                                                                                        Score 111;
Pred. No. 0.
                                                                                                                                                                                                                                                                                                                                                                                                                     mature ChIL-6.
; 657F8049F25BD2F8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Potential
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Craniata; Vertebrata; Eutel; Galliformes; Phasianidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sequence update)
annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Salmonella
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   avian cells in response to
Salmonella enteritidis and
233
                                       172
                                                                                 ---INPDEVVIP--DSAAQKSLLANLKSDKDW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Barrow P.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      241
                                                                                                                                                                                                                                                                                                                            74;
                                                                                                                                                                                                                                                                                                                                                                                띪
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ጅ
                                                                                                                                                                                                                                                                                                                                                                            2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                databases
                                                                                                                                                                                                                                                                                                                                                                            Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IEA.
                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Burnside
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                241;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Phasianinae;
                                                                                                                                                                                                                                                                                                                                      52;
                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                   206
                                                                                                                             153
                                                                                                                                                                    156
                                                                                                                                                                                                              99
                                                                                                                                                                                                                                                       100
                                                                                                                                                                                                                                                                                               44
```

```
DRRITA X PRINCIPLE TO THE PRINCIPLE OF T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 14
Q8MJ75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 15
Q9XT80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 á
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         र्
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A CONTRACTOR OF THE CONTRACTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
EMBL; AF076643; AAD42929.1; HSSP; P05231; 1ALU.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q9XT80;
                                                                                                   MEDLINE=20141864; PubMed=10678396; DOI=10.1016/S0165-2427(99)00150-6; St-Laurent G., Archambault D.; St-Laurent rolning, phylogenetic analysis and expression of beluga whale (Delphinapterus leucas) interleukin 6."; Vet. Immunol. Immunopathol. 73:31-44(2000).
                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                           Delphinapterus leucas (Beluga whale).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Cetartiodactyla; Cetacea; Odontoceti;
Monodontidae; Delphinapterus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q8MJ75;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-NOV-1999
01-MAR-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRINTS; PRO0433; ILGGCSFMGF.
PRINTS; PRO0434; INTERLEUKIN6.
PRODOM; PD004356; Interleukin 6; 1.
SMART; SM00126; ILG; 1.
PROSITE; PS00254; INTERLEUKIN 6; 1.
SEQUENCE 212 AA; 23881 MW; 1F54
                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=9749;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR009079; 4 helix_cytokine.
InterPro; IPR003573; II6_MGF_GCSF.
InterPro; IPR003574; Interleukin_6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AF518322; AAM74938.1; HSSP; P05231; 1ALU.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.

Lee D., Yoo H., Choi I.;

Submitted (JUN-2002) to the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-OCT-2002
01-OCT-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00489; IL6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sus scrofa (Pig).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             nterleukin 6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=9823;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local
P; P05231; IALU
GO:0005576; C:extracellular; IEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GO:0005138; F:interleukin-6 receptor GO:0006955; P:immune response; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GO:0005125; F:cytokine activity; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GO:0005576; C:extracellular; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    172 NAGLLDKLOSONEWMKNTKIILILRSLEDFLOFSLRAIR 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
37; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LMRITTGLVEFQIYLDYLQKEYESNKGNVEAVQISTKALIQTLRQKGKNPDKATTPNPTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KTEELIKYILGKISAMREEMCEKYEKCENSKEVLAENNLNLPKMAEKDGCFQSGFNQETC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KCLEQVRKIQGDGAALQEKLCATYKLCHPEELVLLGHSLGIP-WAPLSSCPSQALQLAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LSQLHSGLFLYQGLLQALEGISPELGPTLDTLQLDVADFATTIWQQMEELGMAPALQPT-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -QGAMPAFAS--AFQRRAGGVLVASHLQSFLEVSYRVLR 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (TrEMBLrel. (TrEMBLrel. (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (TrEMBLrel. (TrEMBLrel. (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chordata; Craniata; Vertebrata; Cetartiodactyla; Suina; Suidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12.3%; Sc
23.3%; Pr
1tive 32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12,
12,
26,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Created)
Last seq
Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 110.5;
Pred. No. 0.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1F540E7030BCFD77 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0.053;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ₽
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                85;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Buteleostomi;
Sus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   212;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   <u>ت</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   75
```

```
Ś
                                                      멍
                                                                             Ś
                                                                                                           밁
                                                                                                                                  Ś
                                                                                                                                                                                                                       Query Match
Best Local (
                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                            GO; GO:000
GO; GO:000
GO; GO:000
InterPro;
                                                                                                                                                                                                                                  ProDom; PD004356; Int
SMART; SM00126; IL6;
PROSITE; PS00254; INT
                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                             PRINTS; PR00434; INTERLEUKIN6.
                                                                                                                                                                                                                                                                                         PRINTS; PR00433; IL6GCSFMGF
                                                                                                                                                                                                                                                                                                                    InterPro; IPR003574;
                                                                                                                                                                                                                                                                                                                              InterPro; IPR009079; 4_helix_cytokine.
InterPro; IPR003573; IL6_MGF_GCSF.
                                                                                                                                                                                                                                                                                                                                                            GO:0005125; F:cytokine activity; IEA.
GO:0005138; F:interleukin-6 receptor binding; IEA.
GO:0006955; P:immune response; IEA.
 172
                           138
                                                      112
                                                                                81
                                                                                                           52
                                                                                                                                   22 VRKIQGDGAALQEKLCATYKLCHPEELVLLGHSLGIP-WAPLSSCPSQALQLAGCLSQLH
                                                                                                                                                                33;
                                                                                                                                                                               Similarity
NNLQSQNDDWMRNTKIILILRSLENFLQFSLRAVR
                           --MPAFASAFQRRAGGVLVASHLQSFLEVSYRVLR 170
                                                                                SGLFLYQGLLQALEGISPELGPTLDTLQLDVADFATTIWQQMEELGMAPALQPTQGA---
                                                   TGLLEYQIYLDYLQNEYEGDKGSIEAVQISIKALAQILRQKVKNPDEVTTPDPTTNASLM 171
                                                                                                             IKYILGKISAMRKEMCEKYDKCENSKEALAENNLNLPKMAEKDGCFQSGFNQETCLMRIT
                                                                                                                                                                                                                     208 AA;
                                                                                                                                                                  Conservative
                                                                                                                                                                                                                     INTERLEUKIN_6; 1.
; 23456 MW; 81CC85C6E80389C4 CRC64;
                                                                                                                                                                                                                                                             Interleukin_6; 1.
                                                                                                                                                                             12.0%;
21.3%;
                                                                                                                                                                                                                                                                                                                 Interleukin_6.
                                                                                                                                                                  35;
                                                                                                                                                                               Pred. No.
                                                                                                                                                                               Score 108; DB 2;
Pred. No. 0.088;
                                                                                                                                                                Mismatches
                                                                                                                                                                  81;
                                                                                                                                                                                          Length 208
                                                                                                                                                                  Indels
                                                                                                                                                                6
                                                                                                                                                                Gaps
                                                                                                                                      80
                                                                                   137
                                                                                                             111
```

Search completed: July 9, 2005, 12:39:03 Job time: 112.318 secs